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STIC-Biotech/ChemLib

From: Elliott, George
Sent: Tuesday, March 14, 2000 8:47 AM
To: STIC-Biotech/ChemLib
Cc: Hamud, Fozia
Subject: FW: rush search 09/167,705

Please rush.

Thanks,

George

-----Original Message-----

From: Hamud, Fozia
Sent: Tuesday, March 14, 2000 8:17 AM
To: Elliott, George
Subject: rush search 09/167,705

Good morning Mr. Elliot, 09/167,705 is an amended case due this Bi-week. I would like to request rush search. Thanks. Please search SEQ ID NO:s 1 and 2 against commercial data bases and please conduct interference search for both sequences. Thanks.

Fozia Hamud
Art Unit 1646
Crystal-Mall-One, Room 10D06
308-8896

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 14, 2000, 15:45:53 ; Search time 216.93 Seconds
(without alignments)
-5478.334 Million cell updates/sec

Title: US-09-167-705-1

Perfect score: 395
Sequence: 1 atgactaagctgagagacca.....agcaaaaaaaaaaaaaa 395

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 821193 seqs, -1518192014 residues

tal number of hits satisfying chosen parameters: 1642386

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

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1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
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6: gb_ph:*
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8: gb_pl2:*
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25: em_ph:*
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46: em_hc1:*
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48: em_hc3:*
49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	319.2	80.8	405	10	AF011757
2	304	77.0	429	3	D49548
3	304	77.0	429	24	E12013
4	304	77.0	429	24	E12020
5	164.4	41.6	441	24	E12012
6	164.4	41.6	442	9	D49549
7	164.4	41.6	461	9	HSCALGRAN
8	164.4	41.6	466	9	D83664
9	129.2	32.7	355	3	AF091848
10	87.2	22.1	598	4	GG126MRP
11	86	21.8	532	9	HSS1002
12	86	21.8	4992	9	D83657
13	86	21.8	111213	45	AC011666
14	83.6	21.2	480	3	AF091849
15	81	20.5	287	9	HSS1003
16	75.6	19.1	336	5	A12024
17	75.6	19.1	462	5	A12029
18	75.6	19.1	462	9	HSMRP14
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21	75.6	19.1	571	5	AR015928
22	69.6	17.6	1488	12	RATSI00B
23	69.6	17.6	1488	12	RATSI00P
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25	65.4	16.6	488	3	D89056
26	64.8	16.4	273	13	G24223
27	63.8	16.2	283	14	SYNS100SYN
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29	61.4	15.5	284	5	A12022
30	61.4	15.5	408	5	AR015927
31	61.4	15.5	418	5	I93571
32	61.4	15.5	418	9	HSMRP8
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35	61.2	15.5	487	12	RATSI00RO
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42	59	14.9	303	5	AR037321
43	58.8	14.9	303	5	AR062122
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ALIGNMENTS

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LOCUS AF011757
DEFINITION Homo sapiens RAGE binding protein (P12) mRNA, complete cds.
ACCESSION AF011757
VERSION AF011757.1 GI:2293532
KEYWORDS

Source	Organism	Human
REFERENCE	Authors	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Title	1 (bases 1 to 405)
REFERENCE	Journal	Li, J.F., ... Hofmann, M.A., Drury, S., Qu, X. and Schmidt, A.M. Functional identification of a novel ligand for RAGE Unpublished
REFERENCE	Authors	2 (bases 1 to 405)
REFERENCE	Title	Li, J.F., ... Hofmann, M.A., Drury, S., Qu, X. and Schmidt, A.M. Direct Submission
REFERENCE	Journal	Submitted (30-JUN-1997) Physiology, Columbia University, 630 W. 168th St., New York, NY 10032, USA
FEATURES	Source	Location/Qualifiers
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		/tissue_type="lung"
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		/db_xref="GI:2293533"
		/translation="WTKLEHLEGIINIFHOYSVRVGHFDLTKRELQITKELPKT LQNKDQPTIDKIFQDDLDADRDKGAVSFEEFVILVSRVLTAKHIDHKE"
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Matches 386; Conservative	0; Mismatches 8; Indels 12; Gaps 5;	
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DB	180 cctgtagatcgctgtaagaagcggtcgatgctgtaggaatctgtagtctggtccag	240
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DB	240 ggtgtgaaaagagccacatagatcatccaaagaagtagt-----tttcagaagat	294
QY	295 tcccaagaagacttaccctctcctccctcctgagctgctg-----ctcccgagagga	351
DB	300 ccccaagaagacttaccctctcctccctcctgagctgctg-----ctcccgagagga	351
QY	352 -ataagctactctggcaaa-ttcttagcaaaaaaataaaaaa 395	
DB	360 aataaacgacttctggcaaa-gttttagcaaaaaaataaaaaa 405	
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LOCUS	D49548	429 bp mRNA
DEFINITION	Bos taurus mRNA for calcium-binding protein in amniotic fluid 1, complete cds.	10-FEB-1999
ACCESSION	D49548	
VERSION	D49548.1	GI:1694616
KEYWORDS	CAAF1, calcium-binding protein in amniotic fluid 1.	

SOURCE	Bos taurus fetus esophagus cDNA to mRNA, clone_jlb:fetal bovine esophagus cDNA.
ORGANISM	Bos taurus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
AUTHORS	Hitomi,J.
TITLE	Direct Submission
JOURNAL	Submitted (09-MAR-1995) to the DDBJ/EMBL/GenBank databases, Jiro Hitomi, National Cancer Center Research Institute, Growth Factor Division, 5-1-1 Tsukiji, Chuoh-Ku, Tokyo 104, Japan (Tel:03-3542-2511, Fax:03-3542-8170)
REFERENCE	Hitomi,J.
AUTHORS	2 (bases 1 to 429)
JOURNAL	Unpublished (1996)
REFERENCE	3 (sites)
AUTHORS	Hitomi,J., Yamaguchi,K., Kikuchi,Y., Kimura,T., Murayama,K. and Nagasaki,K.
TITLE	A novel calcium-binding protein in amniotic fluid, CAAF1: its molecular cloning and tissue distribution
JOURNAL	J. Cell. Sci. 109 (Pt 4), 805-815 (1996)
MEDLINE	96298783
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	/db_xref="taxon:9913"
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	/dev_stage="fetus"
	/tissue_type="esophagus"
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QY	61 cgagtgaggcatcttcgacacccctacaagcgctgaagcgtgatcacaaaagga 120
Db	108 CGGCGGGGGCAATTTGCACACCTCAACAAGGTGAGTGAAAGCACGTCATCAAAA-GGA 166
QY	121 acttccccaaaaocctccggagaacccaagaacacaactccattgcacaaatatctccaaga 180
Db	167 ACTTCCCAAAAACCCCTCCAGAACACCCAAGATCAACCTACCATGTGACAAATAATTCCAAGA 226
QY	181 cctggaatgcgataaagaacggagccgctgaagctttgaagaaatctcgtagtcctgtgtlccag 240
Db	227 CCTGATGCCGATTAAGAAGCGAGCGCGCTGACGTTTAGGAATTCGTAAGTCTTGCTGCCAG 286
QY	241 ggtagctgaanaaacgccacatagatatccacaagaagtagg-----ttccagaatgtc 294
Db	287 GGTTGTTGAAAAACGCCACATAGATATCCAAATAAGTAGMAAGCTCTTTCCAGCAATGT 346
QY	295 tcaccaagaagaacttaaccctctcctcccctgaagcgtgc---tcgccgagggagaagaat 351
Db	347 CCCCAAGAAAGACTTRACCTTCTCTCTCCTGAGGCTGCTTACCCGAGGAGAGAGAAATT 406
QY	352 -ataaagctactttgccaatt 372

DB 407 AATAACGTAAGTGGCAAGT 428

RESULT 3

ID E12013 standard; RNA; MAN; 429 BP.

XX E12013;

XX E12013.1

XX 07-OCT-1997 (Rel. 52, Created)

XX 08-OCT-1997 (Rel. 52, Last updated, Version 1)

DE cDNA encoding bovine CAAFI (Calcium binding protein in Amniotic Fluid

DE 1).

XX JP 1996238090-A/2.

XX Bos taurus

XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;

XX Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

XX [1]

XX 1-429

XX Hitomi J., Yamaguchi K., Yamamura T.;

XX "NEW CALCIUM-BINDING PROTEIN";

XX Patent number JP 1996238090-A/2, 17-SEP-1996.

XX HITOMI JIRO, TONEN CORP.

XX OS Bos taurus (bovine)

XX PN JP 1996238090-A/2

XX PD 17-SEP-1996

XX PF 06-MAR-1995 JP 1995045564

XX PI HITOMI JIRO, YAMAGUCHI KEN, YAMAMURA TOKUSHICU

XX PC C12N15/09, C07H21/04, C07K14/47, C07K19/00, C12N1/15, C12N1/19,

XX C12N1/21,

XX PC C12N5/10, C12P21/02, C12P21/08, G01N33/53, G01N33/574,

XX G01N33/577//A61K39/395,

XX A61K39/395, (C12N1/15, C12R1:69), (C12N1/19, C12R1:865), (C12N1/21,

XX C12R1:19),

XX PC (C12P21/02, C12R1:19), (C12P21/08, C12R1:91);

XX CC strandedness: Double;

XX CC topology: Linear;

XX CC hypothetical: No;

XX CC anti-sense: No;

XX FH Key

XX FH source

XX FH 1. .429

XX FH /organism="Bos taurus"

XX FH /cell-type="Amniotic fluid"

XX FH 5'UTR

XX FH 1. .47

XX FH CDS

XX FH 48. .326

XX FH /product="Bovine CAAFI (Calcium binding protein

XX FH in Amniotic

XX FH Fluid 1)"

XX FH 3'UTR

XX FH 327. .429

XX FH Location/Qualifiers

XX FH key

XX FH 1. .429

XX FH /db_xref="taxon:9913"

XX FH /organism="Bos taurus"

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QY 61 cgagtgaggcatttcgagacccttcacaaagcgtagctgaagcagctgatacaaaagga 120

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DB 108 CGGGTGGGGCATTTTCGACACCCCTTACACAGCGTGAAGCTGATCACAAG- GGA 166

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QY 121 acttcccaaaaccccttcagagacacacaaagacacacacatgcagaaatattccaaga 180

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DB 167 ACTTCCAAAACCTTCAGAAACACCAAGATCAACCTACCATTCACAAATATTCACAGA 226

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QY 181 cctgtagccgataaagagagcgcgcagcttgaggaattgtagtctgctgctcag 240

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DB 227 CTTGGATGCCGATTAACCGAGCGCTCAGCTTGAGGAATTCGTAGTCTGTGTCTCAG 286

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QY 241 ggtctgtaaaacagccacatagatccacaagagtagg-----ttccagcaatgt 294

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DB 287 GGTCTGAAAACAGCCCATAGATATCCACAAAGATAGGAAGCTTTTCCACCAATGT 346

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QY 295 tcccaagaagactaccccttcctccctgagctgc---tcccgagaggaagagaatt 351

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QY 352 -ataagctacttgccaatt 372

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DB 407 AATAACGTAAGTGGCAAGT 428

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XX E12020;

XX AC E12020;

XX SV E12020.1

XX 08-OCT-1997 (Rel. 52, Created)

XX 08-OCT-1997 (Rel. 52, Last updated, Version 1)

DE cDNA encoding bovine CAAFI (Calcium binding protein in Amniotic Fluid

DE 1).

XX JP 1996238091-A/1.

XX OS Bos taurus

XX PN JP 1996238091-A/1

XX PD 17-SEP-1996

XX PF 06-MAR-1995 JP 1995070468

XX PI HITOMI JIRO, YAMAGUCHI KEN, KIMURA TATSUJI

XX PC C12N15/09, C07H21/04, C07K14/47, C07K16/18,

XX C12N1/21,

XX PC C12P21/02, C12P21/08, G01N33/53, G01N33/577//A61K39/395,

XX A61K39/395,

XX PC C12N5/10, (C12N1/21, C12R1:19), (C12P21/02, C12R1:91), (C12P21/02,

XX C12R1:19),

XX PC (C12P21/08, C12R1:91), (C12N5/10, C12R1:91);

XX CC strandedness: Double;

XX CC topology: Linear;

XX CC hypothetical: No;

XX CC anti-sense: No;

XX FH Key

XX FH source

XX FH 1. .429

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CC FT 3'UTR
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FH source
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FT /db_xref="taxon:9913"
FT /organism="Bos taurus"
SQ Sequence 429 BP; 130 A; 111 C; 97 G; 91 T; 0 other;

Query Match
Best Local Similarity 94.5%; Score 304; DB 24; Length 429;
Matches 361; Conservative 0; Mismatches 10; Indels 11; Gaps 4;

QY 1 atgactaagctggagagccaccctggagaggaatcacaatcttcacacagtaactcgtt 60
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QY 61 cgggtggggaattcgacacccctcaacaagcgtgagctgaagcagctgatacaaaagga 120
DB 108 CGGGTGGGCAATTTCGACACCCCTCAACAGCGTGAAGCGTGAAGCGATCACAAG- 166
QY 121 acttcccaaaacccctcagaagaacacaaagacacacacacacacacacacacacacac 180
DB 167 ACTTCCCAAAACCCCTCAGAACACCAAGATCAACCTACATTGACAAATATTCACAGA 226
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QY 352 -ataaagctacttggaatt 372
DB 407 AATTAACGTAATTGGCAAGT 428

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AC E12012;
SV E12012.1
DT 07-OCT-1997 (Rel. 52, Created)
DT 08-OCT-1997 (Rel. 52, Last updated, Version 1)
DE cDNA encoding human CArF1 (Calcium binding protein in Amniotic fluid
DE 1).
XX JP 1996238090-A/1.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
XX Primates; Catarrhini; Hominoidea; Homo.
XX [1]
XX 1-441
RP

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RA Hitomi J., Yamaguchi K., Yamamura T.;
RT "NEW CALCIUM-BINDING PROTEIN";
RL Patent number JP 1996238090-A/1, 17-SEP-1996.
XX HITOMI JIRO, TONEN CORP.

CC OS Homo sapiens (human)
CC PN JP 1996238090-A/1
CC PD 17-SEP-1996
CC PF 06-MAR-1995 JP 1995045564
CC PI HITOMI JIRO, YAMAGUCHI KEN, YAMAMURA TOKUSHIROU
CC PC C12N1/09,C07H21/04,C07K14/47,C07K19/00,C12N1/15,C12N1/19,
CC PC C12N1/21,
CC PC C12N5/10,C12P21/02,C12P21/08,G01N33/53,G01N33/574,
CC PC G01N33/577//A61K39/395,
CC PC A61K39/395,(C12N1/15,C12R1:69),(C12N1/19,C12R1:865),(C12N1/21,
CC PC C12R1:19),
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CC CC strandedness: Double;
CC CC topology: Linear;
CC CC hypothetical: No;
CC CC anti-sense: No;
CC CC Key
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CC FT CDS
CC FT 22..300
CC FT /product="Human CArF1 (Calcium binding protein
CC FT in Amniotic
CC FT Fluid 1)"
CC FT 301..441
CC FT 3'UTR
FH Key
FH source
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FT /organism="Homo sapiens"
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QY 61 cgggtggggaattcgacacccctcaacaagcgtgagctgaagcagctgatacaaaagga 120
DB 82 CGGAAGGGCAATTTTGACACCTCTCTTAAGGTGAGCTGAAGCAGCTGTTACAAA-GGA 140
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QY 181 cctggatgccgataaagacagcgcgtcagcttgaagaaattgtagctggtgtcag 240
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DB 261 TGGCTGAAGGCTGCCCATTAACCAACCCCAAGAGATAGT 302

RESULT 6
D49549 442 bp mRNA PRI 10-FEB-1999
LOCUS D49549
DEFINITION Homo sapiens mRNA for calcium-binding protein in amniotic fluid 1,
complete cds.

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ORIGIN

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Best Local Similarity 83.1%; Pred. No. 3.6e-14;
Matches 98; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 atgactaaagctggagagaccactggagggaatcatcaacattccacagtaactccggt 60
DB 3006 ATGACAAACTTGAGAGAGCATCTGGAGGGAATTGTCATATCTTCACCAATCTCAGTT 3065
QY 61 cgggtggggcatttcgacacccctcaacaagcgtgagctgagagctgtatcacaaag 118
DB 3066 CGGAGGGGCATTTCGACACCTCTCTAAGGCTGAGAGCTGCTTACCAAGG 3123

RESULT 13
AC011666 111213 bp DNA HTG 08-DEC-1999
LOCUS Homo sapiens, *** SEQUENCING IN PROGRESS *** 23 unordered pieces.
DEFINITION AC011666.8 GI:6532064
ACCESSION AC011666.8
VERSION HTG; HTGS-PHASE1.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 111213)
AUTHORS Malaj,E., Wang,Q., Cowell,J.K. and Roe,B.A.
TITLE Home sapiens Chromosome 1q21 BAC Clone 236c22
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 111213)
AUTHORS Malaj,E., Wang,Q., Cowell,J.K. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (09-OCT-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT On Dec 7, 1999 this sequence version replaced g1:6272402.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 3202: contig of 3202 bp in length
* 3203 3265: gap of unknown length
* 3266 3405: contig of 2140 bp in length
* 3406 3468: gap of unknown length
* 3469 8077: contig of 2609 bp in length
* 8078 8140: gap of unknown length
* 8141 11115: contig of 2975 bp in length
* 11116 11178: gap of unknown length
* 11179 14012: contig of 2834 bp in length

* 14013 14075: gap of unknown length
* 14076 16747: contig of 2672 bp in length
* 16748 16810: gap of unknown length
* 16811 18967: contig of 2157 bp in length
* 18968 19030: gap of unknown length
* 19031 22983: contig of 3953 bp in length
* 22984 23046: gap of unknown length
* 23047 27364: contig of 4318 bp in length
* 27365 27427: gap of unknown length
* 27428 31602: contig of 4175 bp in length
* 31603 31665: gap of unknown length
* 31666 36610: contig of 4945 bp in length
* 36611 36673: gap of unknown length
* 36674 41511: contig of 4838 bp in length
* 41512 41574: gap of unknown length
* 41575 45836: contig of 4262 bp in length
* 45837 45899: gap of unknown length
* 45900 50569: contig of 4670 bp in length
* 50570 50632: gap of unknown length
* 50633 56029: contig of 5397 bp in length
* 56030 56092: gap of unknown length
* 56093 61590: contig of 5498 bp in length
* 61591 61653: gap of unknown length
* 61654 67822: contig of 6169 bp in length
* 67823 67884: gap of unknown length
* 67885 73338: contig of 5454 bp in length
* 73339 73400: gap of unknown length
* 73401 78323: contig of 4923 bp in length
* 78324 78385: gap of unknown length
* 78386 83693: contig of 5308 bp in length
* 83694 83756: gap of unknown length
* 83757 91520: contig of 7765 bp in length
* 91521 91582: gap of unknown length
* 91583 100475: contig of 8893 bp in length
* 100476 100537: gap of unknown length
* 100538 111213: contig of 10676 bp in length.

FEATURES
Source location/Qualifiers
1..111213
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 31120 a 23925 c 25160 g 29624 t 1384 others
ORIGIN

Query Match 21.8%; Score 86; DB 45; Length 111213;
Best Local Similarity 83.1%; Pred. No. 4.4e-14;
Matches 98; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 atgactaaagctggagagaccactggagggaatcatcaacattccacagtaactccggt 60
DB 23516 ATGACAAACTTGAGAGAGCATCTGGAGGGAATTGTCATATCTTCACCAATCTCAGTT 23575
QY 61 cgggtggggcatttcgacacccctcaacaagcgtgagctgagagctgtatcacaaag 118
DB 23576 CGGAGGGGCATTTCGACACCTCTCTAAGGCTGAGAGCTGCTTACCAAGG 23633

RESULT 14
AF091849 480 bp mRNA MAM 29-SEP-1998
LOCUS Oryctolagus cuniculus calgranulin B mRNA, partial cds.
ACCESSION AF091849
VERSION AF091849.1 GI:3661598
KEYWORDS
SOURCE Oryctolagus cuniculus.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 480)
AUTHORS Yang,Z., deVeer,M.J., Gardiner,E.E., Devenish,R.J., Handley,C.J.,
TITLE Underwood,J.R. and Robinson,H.C.
Rabbit polymorphonuclear neutrophils form 35S-labeled
S-sulfo-calgranulin C when incubated with inorganic [35S]sulfate

GenCore version 4.5
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OK nucleic - nucleic search, using sw model

Run on: March 14, 2000, 15:47:30 ; Search time 56.66 seconds
(without alignments)
1744.191 Million cell updates/sec

Title: US-09-167-705-1

Perfect score: 395
Sequence: 1 atgactaagctggaggacca.....agcaaaaaaaaaaaaaaa 395

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: (623170)

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	304	77.0	429	1 T39345	Calcium binding pr
2	166	42.0	273	1 T62569	DNA encoding compo
3	164.4	41.6	440	1 T39346	Calcium binding pr
4	164.4	41.6	479	1 T85774	Human chemotactic
5	75.6	19.1	571	1 V34698	Human calprotectin
6	63.8	16.2	150	1 V87807	EST clone EH78. Ne
7	61.4	15.5	408	1 V34697	Human calprotectin
8	59	14.9	303	1 Q20506	Human mts-1 coding
9	59	14.9	303	1 Q99177	Human mts-1 gene.
10	58.8	14.9	4440	1 T68322	Human multidrug re
11	54.2	13.7	579	1 Q99178	Human mts-1 CDNA.
12	53.4	13.5	488	1 T20500	Human gene signatu
13	51.6	13.1	433	1 Q23343	Murine CP-10. New
14	49.8	12.6	4195	1 T68321	Human multidrug re
15	41.8	10.6	10952	1 T33345	Human CAPL gene.
16	41.8	10.6	10952	1 V41162	Human CAPL gene.
17	41.8	10.6	10952	1 X17696	Human CAPL genomic
18	41.6	10.5	254	1 T20087	Human gene signatu
19	39.6	10.0	350	1 X23464	Human neutrophil c
20	35.2	8.9	452	1 Q28007	Sequence encoding
21	35.2	8.9	452	1 Q28007	Sequence of clone
22	35.2	8.9	452	1 Q28007	EST clone J635. Ne
23	34	8.6	1080	1 V73498	Human S100P1 DNA.
24	33.8	8.3	447	1 Q04331	Recombinant calmod
25	32.8	8.3	504	1 Q04332	Plasmid pOCAL7 con
26	32.8	8.3	654	1 Q04332	Plasmid pOCAL7 con
27	32.4	8.2	4160	1 V41884	Nucleotide sequence
28	31.8	8.1	861	1 Q99552	Thrombospondin cod
29	31.4	7.9	3175	1 V34323	Human secreted pro
30	31.2	7.9	3259	1 V34306	Human secreted pro
31	31.2	7.9	243	1 Q57430	Ca binding protein
32	31.2	7.9	532	1 T85298	Human Chemotactic
33	31.2	7.9	673	1 X39799	Gastric cancer ass
34	31.2	7.9	1141	1 V73499	Human S100P2 DNA.

35	31.2	7.9	1543	1 X27326	Human secreted pro
36	31.2	7.9	110000	1 V30458.1	Continuation (2 of
c 37	31.2	7.9	110000	1 V30459.1	Continuation (2 of
38	31	7.8	2349	1 V80608	Kidney injury asso
39	31	7.8	4590	1 N60472	Sequence encoding
c 40	30.8	7.8	573	1 X39800	Gastric cancer ass
41	30.6	7.7	173	1 V00432	3' fragment of clo
42	30.6	7.7	173	1 T91309	Human H83-22 secre
43	30.6	7.7	463	1 Q68827	hg14 clone showing
44	30.6	7.7	1078	1 T91308	Human H83-22 secre
45	30.6	7.7	5194	1 X25885	C.albicans alpha-I

ALIGNMENTS

RESULT 1	
T39345	T39345 standard; CDNA; 429 BP.
AC T39345;	
DT 01-MAY-1997 (first entry)	
DE Calcium binding protein CAAP1 coding sequence.	
KW Calcium binding protein; bovine; amniotic fluid; S100 protein family;	
KW Intracellular signal transduction; squamous epithelial cell; neutrophil;	
KW macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;	
KW squamous cell carcinoma; skin; oesophagus; CAAP1; lung; blood disease;	
KW ds.	
OS Bos taurus.	
FH Key	Location/Qualifiers
FT cds	48..326
FT	/*tag= a
FT	/product= calcium binding protein

EP-731166-A2.

11-SEP-1996.
04-DEC-1995; 119045.
06-MAR-1995; JP-070468.
06-MAR-1995; JP-045564.
(HIRO) HIROMI J.
PA (TOFU) TONEN CORP.
PI Hitomi J, Kimura T, Yamaguchi K, Yamamura T;
DR WPT; 96-403989/41.
DR P-PSDB; W03563.

PR - New human or bovine calcium binding protein and related nucleic acid
PT - is a marker for inflammation, neoplasia, skin and blood diseases
PS Claim 1: Page 21; 36pp; English.
CC This sequence represents the coding sequence for the CAAP1
CC calcium-binding protein isolated from bovine amniotic fluid. CAAP1
CC belongs to the S100 protein family, which includes calyculin, MRP8, and
CC MRP14. Intracellular calcium ion concentration is one of the key factors
CC for intracellular signal transduction. The calcium signals are
CC transduced by various calcium-binding proteins, such as the protein
CC encoded by this sequence. CAAP1 is normally expressed in squamous
CC epithelial cells, neutrophils and macrophages, but atypical epithelial
CC cells are negative for CAAP1 and overexpression is observed in several
CC types of cancer cells and neutrophils/macrophages infiltrating cancerous
CC lesions. Detection of CAAP1 (using antibodies in usual immunoassays) can
CC be used to diagnose (or monitor) inflammation, neoplasia (particularly
CC squamous cell carcinoma of the skin, oesophagus, lung and cervix), and
CC skin and blood diseases.

SQ Sequence 429 BP; 130 A; 111 C; 97 G; 91 T;

Query Match 77.0%; Score 304; DB 1; Length 429;
Best Local Similarity 94.5%; Fred. No. 7.6e-81;
Matches 361; Conservative 0; Mismatches 10; Indels 11; Gaps 4;

QY 1	atgactaagctggaggaccacctggaggaatcatcacaatcttcacacagatccgtt 60
DB 48	atgactaagctggaggaccacctggaggaatcatcacaatcttcacacagatccgtt 107
QY 61	cgggtgggagcatttcgacacccctcaacaagcgtgagctgaagcagctatcacaagaagga 120
DB 108	cgggtgggagcatttcgacacccctcaacaagcgtgagctgaagcagctatcacaagaagga 166

[illegible]

```

1001 ID T62569
1002 AC T62569 standard; DNA; 273 BP.
1003 DE 16-Oct-1997 (first entry)
1004 DE DNA encoding component of bioactive metal RNA polypeptide.
1005 KM Bioactive; metal; RNA polypeptide; RNP; modulation; analysis;
1006 KM angiogenesis; vascular state; mammalian tissue; transfer; cell;
1007 KM genetic information; selective; alteration; nucleic acid content;
1008 KM leukocyte; pig; monocytic-RNAP; ss.
1009 KM Sus scrofa.
1010 FH Key
1011 FT mat_peptide Location/Qualifiers
1012 FT 1..272 /*tag= a
1013 PN DE1628895-A1.
1014 PD 23-JAN-1997.
1015 PE 17-JUL-1996; 028895.
1016 PR 18-AUG-1995; DE-030500.
1017 PR 17-JUL-1995; DE-025992.
1018 PA (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
1019 PA Hellmeyer LMG, Kieseewetter S, Logemann E, Wislser JH;
1020 PI WPI; 97-088586/09.
1021 DR P-PSDB: W01826.
1022 PT Bioactive metal RNA polypeptide - useful for modulating
1023 PT angiogenesis, etc.
1024 PS Disclosure; Page 2; 16pp; German.
1025 CC A novel bioactive metal RNA polypeptide (RNP) has a RNA component
1026 CC including the sequence T62568 and a polypeptide component having
1027 CC the sequence W01826, which is encoded by T62569. The RNP, or
1028 CC anti-RNP immunoglobulins, can be used to modulate and/or analyse
1029 CC angiogenesis and the vascular state of mammalian tissue, transfer
1030 CC genetic information in cells and selectively alter the nucleic
1031 CC acid content of cells.
1032 CC Leukocytes from pig's blood were cultured in medium, and the
1033 CC supernatant treated with NH4 sulphate at 35, 45 and 90% saturation
1034 CC to precipitate protein fractions. The residual supernatant was
1035 CC diluted to 45% NH4 sulphate saturation and concentrated by
1036 CC ultrafiltration using a 0.5 kD membrane. The retentate was purified
1037 CC to give 8 mg of product described as monocytic-RNAP.
1038 CC Sequence 273 BP; 77 A; 78 C; 72 G; 46 T;

```

Query Match	42.0%	Score 166:	DB 1;	length 273;
Best Local Similarity	77.7%	Pred. No.	4e-40;	
Matches 213; Conservative	0;	Mismatches	60;	Indels 1; Gaps 1;

[illegible]

Db	61	CTGGGGCCACTGTGACACCCTGATCAACGGGAGCTGTAAGCAGCGTGAATACCAAT - GGAAGCT	11.9
QY	124	tccccaaaacccctccagaacacccaagaagccaaacctaccattgacaaaatalctcaagact	183
Db	120	GCCCAACCCCTGTAAGAAACAACAAGSACAGGGGACCATTTGACACAGATCTTCCAGAAACCT	17.9
QY	184	ggaatgcccgaataaagacggaagccgctcgaactttgagaaatcgtatgctctggtgtgtccaggt	24.3
Db	180	GGATGCCCAACGAGATGAGCAGGTGTCTTTCAGAGATTTGTGTGTGTGACAGATGT	23.9
QY	244	gcttgaaaacagcccacacatagatatccacaagaag	27.7
Db	240	GCTGATCACAACCCATGACAAACATCCACAAAGAG - 27.3	

RESULT	3
T39346	
ID	T39346 standard; cDNA; 440 bp.
AC	T39346;
DT	01-MAY-1997 (first entry)
DE	Calcium binding protein CArfl coding sequence.
KW	Calcium binding protein; human; amniotic fluid; S100 protein family;
KW	intracellular signal transduction; squamous epithelial cell; neurophil;
KW	macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;
KW	squamous cell carcinoma; skin; oesophagus; CArfl; lung; blood disease;
KW	ds.
OS	Homo sapiens.
EH	Key
ET	cds
	location/Qualifiers
	22..300

PN EP-731166-A2.
PD 11-SEP-1996.
PE 04-DEC-1995; 119045.
PR 06-MAR-1995; JP-070468.
PR 06-MAR-1995; JP-045564.
PA (HITO/) HITOMI J.
PA (TOFU) TONEN CORP.
PI Hitomi J, Kimura T, Yamaguchi K, Yamamura T;
DR WPI: 96-403989/41.
DR P-PSDB: W03564.
PT New human or bovine calcium binding protein and related nucleic acid
PT - is a marker for inflammation, neoplasia, skin and blood diseases
PS Claim 1; Page 24; 36pp; English.
CC This sequence represents the coding sequence for the CAAFI
CC calcium-binding protein isolated from human amniotic fluid. CAAFI
CC belongs to the S100 protein family, which includes calyculin, MRP8, and
CC MRP14. Intracellular calcium ion concentration is one of the key factors
CC for intracellular signal transduction. The calcium signals are
CC transduced by various calcium-binding proteins, such as the protein
CC encoded by this sequence. CAAFI is normally expressed in squamous
CC epithelial cells, neutrophils and macrophages, but atypical epithelial
CC cells are negative for CAAFI and overexpression is observed in several
CC types of cancer cells and neutrophils/macrophages infiltrating cancerous
CC lesions. Detection of CAAFI (using antibodies in usual immunoassays) can
CC be used to diagnose (or monitor) inflammation, neoplasia (particularly
CC squamous cell carcinoma of the skin, oesophagus, lung and cervix), and
CC skin and blood diseases.
SQ Sequence 440 Bp; 148 A; 98 C; 90 G; 104 T;

Query Match	41.68;	Score 164.4;	DB 1;	Length 440;
Best Local Similarity	76.28;	Pred. No. 1.4e-39;		
Matches 215; Conservative	0;	Mismatches 66;	Indels 1;	Gaps 1

[illegible]

Oy	121	acttcccaaaaccccaccagacaagaacccaatcttacattgacataatattccaaga	180
Oy	121	acttcccaaaaccccaccagacaagaacccaatcttacattgacataatattccaaga	180
Dd	141	GCTTGCACAAACCATTACAGATATCAAGAATATAAGCTGTCAATTGATGAATATTTCCAAG	200
Oy	161	cctgatgcgcgaataaagaagcgccgtcagccttgtaggaattcgtagtctggtgccag	240
Dd	201	CCTGGATGGTATTCAGAACGAGGTGCAGCTTTCCAAAGATCATATCCTGGTAGCAT	260
Oy	241	ggtcgtgaataaacagcccatagatatccacaagaagtgt	282
Dd	261	TGCCGTGAAGGCGTGCCATTACACACCACAAGAAGTAGT	302

RESULT 4

ID	785774	standard; DNA: 479 BP.
NC	785774:	
CD	28-JAN-1998	(first entry)
KW	Human chemotactic cytokine I DNA.	
KW	Chemotactic cytokine; tumour; autoimmune disease; antagonist;	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	76..354	/tag= a
FT	CDS	/product= chemotactic_cytokine_I

```

MO9723640-AI.
03-JUL-1997.
26-DEC-1995: U16871.
26-DEC-1995: WO-U16871.
(HDMA-) HUMAN GENOME SCI INC.
Alfonso P. Gentz R, NI J, SU YJ, YU G;
WP1: 97-351075/32.
P-PSDB: W24137.
DNA encoding Chemotactic cytokine I - used to treat e.g. tumours,
chronic infection, leukaemia, etc.
Claim 4: Pages 48-49; 64pp; English.
This DNA sequence encodes the human chemotactic cytokine I polypeptide.
The DNA was amplified using PCR primers and restriction enzyme sites
were introduced by adding nucleotides corresponding to the chemotactic
cytokine I gene to the 5' and the 3' sequences. The DNA was cloned into
the bacterial expression vector pQE-9, along with a histidine tag and a
RBS. The resulting vector was used to transform the E. coli strain
M15/rep4. The transformants were identified and clones containing the
desired constructs were grown in liquid culture in LB media. The cells
were harvested by centrifugation and solubilised. The chemotactic
cytokine was purified from this solution by chromatography. This
polynucleotide, along with a vector and a host cell can be used for the
recombinant production of the chemotactic cytokine. Cytokine agonists
and antagonists can be used for the treatment of a patient requiring a
chemotactic cytokine I and for the treatment of a patient requiring a
chemotactic cytokine I polypeptide, respectively. The
chemotactic cytokine I is used to treat tumours, chronic infection,
leukemia and T-cell mediated autoimmune diseases.
Sequence 479 BP; 137 A; 113 C; 109 G; 120 T;

```

Query Match 41.6%; Score 164.4; DB 1; Length 479;
Best Local Similarity 76.2%; Pred. No.1.5e-39;
Matches 215; Conservative 0; Mismatches 66; Indels 1; Gaps 1

Dd	1	atgactaaagcgtggaggaccacctggagggaatcatcataactcttcacacagtaactcgtt	60
Dd	76	ATGACAAAACACTTGAGACGATCTGGAGGSAATTTGTAATATCTTCACCAAATNCTAGTT	135
Oy	61	cgggtggtggcatttcgacacccctcaacaagcgtlgagctgaagcaugtgaatcacaaagg	120
Dd	136	CGAAGGGGCGATTGTGACACCCCTCTCTAAGGGGAGACTGAAGCA;CTGCTTACAA-GGA	194
Oy	121	acttcccaaaaccccaccagacaagaacccaatcttacattgaaaaaatattccaaga	180
Dd	195	GCTTGCAACACCATCAAAATATCAAAATATAAGCTGTCAATTGATGAATATTTCCAAG	254

QY	181	ccgtgatccgctaagagagagcgctgacgtttgagagatcgtatcgtgtgcacg	240
DB	255	ccgtgatcgtatcattcaagaaagaaagagctgacgtttcagaattcattccctggtaaccat	314
QY	241	ggttcgtgaanaacagccacatagatattccacaagaagtatg	282
DB	315	tcgcgtgaagagctgcacattaccacacccacaaagagtagt	356
RESULT	5		
ID	V34698	V34698 standard; cDNA; 571 BP.	
AC	V34698:		
DT	03-SEP-1998	(first entry)	
DE	Human calprotectin subunit MRP-14 protein encoding cDNA.		
KW	Human; MRP-8; MRP-14; calprotectin; mineral precipitate; struvite;		
KW	calcium phosphate; kidney stone; renal calculi; struvite stone;		
KW	urinary tract infection; ds.		
OS	Homo sapiens.		
EH	Key	Location/Qualifiers	
ET	CDS	44..385	
ET		/*tag= a	
ET		/product= "human MRP-14"	
PN	US5776348-A.		
PD	07-JUL-1998.		
PF	07-FEB-1995; 385241.		
PR	07-FEB-1995; US-385241.		
PI	(MAST) MASSACHUSETTS INST TECHNOLOGY.		
PI	Asakura H, Dretler SP, Orme-Johnson WH, Selengut JD;		
DR	WPI; 98-397914/34.		
DR	P-PEDB; M60178.		
PT	Inhibiting kidney stone formation - uses the protein calprotectin		
PS	Example 1; Columns 23-24; 19pp; English.		
CC	This cDNA encodes a human calprotectin subunit MRP-14. This is used in		
CC	a method for inhibiting the formation of a mineral precipitate in a		
CC	solution which comprises providing a solution comprising component ions		
CC	of the mineral precipitate or its precursors and contacting the solution		
CC	with an effective amount of isolated calprotectin, or a derivative of it.		
CC	The method is useful for the inhibition of kidney stone formation (renal		
CC	calculi). Kidney stones are concentrations of inorganic and organic salts		
CC	that develop through crystal nucleation, aggregation and growth in the		
CC	kidneys, which then can block the ureter and if not passed to the		
CC	bladder, grow and become symptomatic. Struvite stones (MgNH4PO4) are		
CC	commonly found after urinary tract infection. The mechanisms of this and		
CC	other stone formation is unclear, but some urine compositions are known		
CC	to inhibit formation. One of the major components of these is a protein		
CC	factor calprotectin, which inhibits mineral precipitation. Calprotectin		
CC	can also be used to raise antibodies, which in turn can be used to detect		
CC	the protein in samples. The levels of calprotectin found in samples can		
CC	be compared to levels found in normal humans, and thus assuming increased		
CC	calprotectin correlates to indication of kidney stone formation, this		
CC	procedure can be used as a diagnostic tool.		
SQ	Sequence 571 BP; 160 A; 160 C; 157 G; 94 T;		
Query Match	19.1%;	Score 75.6;	DB 1; Length 571;
Best Local Similarity	59.4%;	Pred No. 2.8e-13;	
Matches 165; Conservative	0;	Mismatches 109;	Indels 4; Gaps 2
QY	1	atgactaaagctgagagacacctgagaggaatcatcatcaatcttcacacagtaactcgt	60
DB	56	atgtgcagacgttgaaagcacaatagagacacatcatcacaacaccttcacacatctgtg	115
QY	61	cgggtggggcatttcgacacccctcaacaagctgtgagctgaagcagctgatacaaaaggga	120
DB	116	aagctggggcaccacccagacaccccttgaaacccgggggaattttaaagagctggt-gcgaa	174
QY	121	attccccaacaaacctccaga--aacccaagacccaactcatgtgacaaatatcca	177
DB	175	tctgcataaattttctcacaagaagagatgaatgaataaagagtcattgaacacatctatgga	234
QY	178	agacctgtgacgcgataaagacgagagcgctcagctttgaggaattcgtgtcctgtgtc	237

DB 235 GGAACCTGGACACAAATGACAGACAGCTGAGCTTCGAGGATCATGCTGATGCG 294
 QY 238 cagggtgctgaanaacagccacacatagatatccacaag 275
 DB 295 GAGGCTAACCTGGGCTCTCCACAGAGAGATGCACGAGG 332

RESULT 6
 ID V87807/c
 AC V87807 standard; cDNA: 150 BP.
 DT 12-FEB-1999 (first entry)

DE EST clone EH78.
 KW Expressed sequence tag; secreted protein; hematopoiesis regulator;
 KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
 KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolytics;
 KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
 OS Homo sapiens.
 PN W09845437.A2.
 PR 15-OCT-1998.
 PR 10-APR-1998; U06956.
 PR 10-APR-1997; US-837312.
 PR (GENY) GENETICS INST INC.

PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Nerberg D,
 PI Racie JA, Spaulding V, Treacy M;
 DR WPI: 99-070078/06.

PT New polynucleotides encoding human secreted proteins - derived from
 PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
 PT ovary, pituitary, retina and colon cDNA libraries

PS Claim 1; Page 186; 641pp: English.

CC The present sequence represents an expressed sequence tag (EST), and is
 CC a polynucleotide of the invention. The polynucleotides of the invention
 CC are all secreted EST sequences isolated from a variety of human tissue
 CC sources. The EST sequences and proteins encoded by them are predicted to
 CC have useful biological activities which would make them suitable for
 CC treating, preventing or ameliorating medical conditions in humans and
 CC animals, although no supporting data is given. Suggested activities
 CC include nutritional activity, immune stimulating or suppressing activity,
 CC haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
 CC activity. The EST sequences are also stated to be useful for gene
 CC therapy.
 SQ Sequence 150 BP; 33 A; 36 C; 33 G; 48 T;

Query Match 16.2%; Score 63.8; DB 1; Length 150;
 Best Local Similarity 74.0%; Pred. No. 5.2e-10;
 Matches 94; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY 88 aagcttgagctgaagcagctgacacaaaggaattcccaaaacctcagaacccaa 147
 DB 146 AGGGGTGACTGAAGCAGCTGCTTACAAA-GGAGCTTGCAAAACCATTAAGATATCA 88
 QY 148 agaccacattacattgacaaataattccaagaacctgagtcgcgataaagcagcg 207
 DB 87 ACATAAAGCTGATGATGAATATTCACAGGCTGATGCAATCAAGATGAAGAGGC 28
 QY 208 cagcttc 214
 DB 27 CGACCTT 21

RESULT 7
 ID V34697
 AC V34697 standard; cDNA: 408 BP.

DT 03-SEP-1998 (first entry)
 DE Human calprotectin subunit MRP-8 protein encoding cDNA.
 KW Human, MRP-8; MRP-14, calprotectin; mineral precipitate; struvite;
 KW calcium phosphate; kidney stone; renal calculi; struvite stone;

KM urinary tract infection; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT 57..338
 FT CDS /tag= a
 FT /product= "human MRP-8"

PN US5776348-A.
 PD 07-JUL-1998.
 PF 07-FEB-1995; 385241.
 PR 07-FEB-1995; US-385241.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PI Asakura H, Dretler SP, Orme-Johnson WH, Selengut JD;
 DR WPI: 98-397914/34.
 DR P-PSDB: W60117.

PT Inhibiting kidney stone formation - uses the protein calprotectin
 PS Example 1; Columns 21-22; 19pp: English.

CC This cDNA encodes a human calprotectin subunit MRP-8. This is used in
 CC a method for inhibiting the formation of a mineral precipitate in a
 CC solution which comprises providing a solution comprising component ions
 CC of the mineral precipitate or its precursors and contacting the solution
 CC with an effective amount of isolated calprotectin, or a derivative of it.
 CC The method is useful for the inhibition of kidney stone formation (renal
 CC calculi). Kidney stones are concentrations of inorganic and organic salts
 CC that develop though crystal nucleation, aggregation and growth in the
 CC kidneys, which then can block the ureter and if not passed to the
 CC bladder, grow and become symptomatic. Struvite stones (MgNH4PO4) are
 CC commonly found after urinary tract infection. The mechanisms of this and
 CC other stone formation is unclear, but some urine compositions are known
 CC to inhibit formation. One of the major components of these is a protein
 CC factor calprotectin, which inhibits mineral precipitation. Calprotectin
 CC can also be used to raise antibodies, which in turn can be used to detect
 CC the protein in samples. The levels of calprotectin found in samples can
 CC be compared to levels found in normal humans, and thus assuming increased
 CC calprotectin correlates to indication of kidney stone formation, this
 CC procedure can be used as a diagnostic tool.
 SQ Sequence 408 BP; 118 A; 91 C; 106 G; 93 T;

Query Match 15.5%; Score 61.4; DB 1; Length 408;
 Best Local Similarity 54.9%; Pred. No. 3.9e-09;
 Matches 151; Conservative 0; Mismatches 111; Indels 13; Gaps 1;

QY 2 tgactaagctgagagaccacactgaggaatcatcaatctccacagctctc 61
 DB 61 TGACCGAGCTGGAGAAACCTTGAACTCATCATGAGCTCAACCAAGTACTCCCTGA 120
 QY 62 gggtagggcatttgacacccctcacaaagcgtagctgaagcagctgatacaaggaa 121
 DB 121 TAAAGGGGAAATTCATGCGCTGTACAGGAGAGACCTTAAGAAATTGCTAGAGACCGAGT 180
 QY 122 ctcccaaaacccctcacagaacacccaagaacacactaccattgacaaataattccaagac 181
 DB 181 GTCCTCAGATATTCAGGAAAGAGGTGCA-----GAGCTGTGTTCAAAAG 227
 QY 182 ctgagtcgcgataaagacgagcgctcagcttgaggaattcgtagctcgtgctcagg 241
 DB 228 TTGGATATCAACACATGATGTCAGTAACTTCCAGGAGTTCCTCATCTGGTATAAG 287
 QY 242 gtagcgtgaaacgcccacatgatattccacaaga 276
 DB 288 ATGGGCGTGGCAGCCCAAAAAAGCCATGAAGA 322

RESULT 8
 ID Q20506
 AC Q20506 standard; cDNA: 303 BP.

DT 14-MAY-1992 (first entry)
 DE Human mts-1 coding region.
 KW Metastatic cancer; antibodies; mouse; lung; liver; kidney; thyroid;
 KW breast cancer; cell growth; 18A2; pRka; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers


```

FT      misc_feature      /note= "conserved DNA motif"
FT      1393..1397        /tag= j
FT      /note= "conserved DNA motif"
FT      1401..1406        /note= k
FT      /note= "conserved DNA motif"
FT      1414..1416        /tag= l
FT      /note= "conserved DNA motif"
FT      1417..1580        /tag= m
FT      /note= "pos: 1431..1433 represents start codon"
FT      Intron            /note= n
FT      1581..3448        /tag= n
FT      /number= 3
FT      misc_feature      /tag= o
FT      1581..1582        /note= "conserved DNA motif"
FT      2738              /tag= p
FT      /note= "N= a 360 nucleotide unsequenced region"
FT      3429..3440        /tag= q
FT      /note= "conserved DNA motif"
FT      3447..3448        /tag= r
FT      /note= "conserved DNA motif"
FT      3449..3826        /tag= s
FT      /number= 3
FT      3667..3685        /tag= t
FT      /note= "conserved DNA motif"
FT      3695..3706        /tag= u
FT      /note= "conserved DNA motif"
FT      3708..3713        /tag= v
FT      /note= "conserved DNA motif"
FT      3723..3727        /tag= w
FT      /note= "conserved DNA motif"
FT      3729..3733        /tag= x
FT      /note= "conserved DNA motif"
FT      3807..3812        /tag= y
FT      /note= "conserved DNA motif"
FT      3827..4440        /tag= z
FT      /number= 4
FT      3837..3842        /tag= aa
FT      /note= "conserved DNA motif"
FT      3844..3845        /tag= ab
FT      /note= "conserved DNA motif"
FT      3847..3848        /tag= ac
FT      /note= "conserved DNA motif"
FT      US5614397-A.      200016.
PD      25-MAR-1997.
PF      22-FEB-1994; 200016.
PR      22-FEB-1994; US-200016.
PA      (STRD ) UNIV LEIAND STANFORD JUNIOR.
PI      Lagasse E, Weissman I;
DR      WPI; 97-224943/20.
DR      P-PSDB; W17062.
PT      Increasing life-span of mammalian haemato-lymphoid cells by
transferring stem cells - with construct contg. cell-specific
transcription initiator and gene encoding protein that increases

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PT      lifetime, useful for drug screening and treatment
PS      Example 1; Column 29-32; 34pp; English.
CC      T68322 is the human MRP14 gene. The transcriptional initiator of this
CC      gene was used in a construct for expressing an open reading frame that
CC      increase the lifespan of a mammalian haematolymphoid cell, e.g. the
CC      mammalian bcl-2 gene, a CFR (cystic fibrosis transmembrane regulator)
CC      gene, the herpes virus thymidine kinase gene or an oncogene.
CC      Haematolymphoid cells are especially neutrophils and the construct
CC      doubles the lifespan of transgenic cells. Transgenic cells or
CC      transgenic animals produced are used for screening for substances and
CC      treatments that prevent or promote cell death. They can also be returned
CC      to the patient to modulate apoptosis, i.e. in the treatment of disorders
CC      related to abnormal cell proliferation or death. Typical applications
CC      are treatment of viral diseases, including HIV; cancer and cystic
CC      fibrosis.
SQ      Sequence 4440 BP; 1099 A; 1203 C; 1159 G; 978 T;

Query Match      14.9%; Score 58.8; DB 1; Length 4440;
Best Local Similarity 68.6%; Pred. No. 5.8e-08;
Matches 81; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

OY      1 atgactaagctggagagaccctggaggaatcatcaacatctccaccagtctcgtt 60
DB      1443 ATGTGCACTGGAGAGCGCACTAGACACATCAACACCTCCACCAATACTCTGTG 1502
OY      61 cgggtgggagcatttcgacacctcaacaagcgtgagctgaagcagctatcacaag 118
DB      1503 AAGCTGGGGGCAACCCAGACACCTGTGACCAAGGGGGAATTCAAGAGCTGTGCGAAGA 1560

RESULT 11
O99178
ID      O99178 standard; cDNA; 579 BP.
AC      O99178:
DE      27-DEC-1995 (first entry)
OS      Human mts-1 cDNA.
OS      Metastasis; cancer; mts-1 gene; tumour; therapy; ds.
OS      Homo sapiens.
PN      W09520656-A1.
PD      03-AUG-1995.
PF      31-JAN-1995; U01214.
PR      31-JAN-1994; US-190560.
PA      (RESE ) RESEARCH CORP TECHNOLOGIES INC.
PI      lukandlin E, zain S;
DR      WPI; 95-275441/36.
PT      Nucleic acid encoding human mts-1, antigenic fragments and
antibodies - useful for diagnosis of malignant cancer and metastatic
potential of tumour cells...
PS      Claim 3; Page 93; 124pp; English.
CC      A human cDNA library was constructed in lambda-gt10 using poly(A)+
CC      RNA prep. from HeLa cells. The library was screened with a 32P-
CC      labeled mouse mts-1 vDNA probe. A clone was obtd. which comprised
CC      the full-length human mts-1 gene (given in Q99177); 3' and 5'
CC      flanking sequences are included in the sequence of O99178. The gene
CC      can be used to express mts-1 protein, e.g. in Sf21 cells, and
CC      antisense constructs are used to inhibit metastasis.
SQ      Sequence 579 BP; 130 A; 149 C; 153 G; 147 T;

Query Match      13.7%; Score 54.2; DB 1; Length 579;
Best Local Similarity 55.0%; Pred. No. 6.1e-07;
Matches 127; Conservative 0; Mismatches 103; Indels 1; Gaps 1;

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DB 267 CTTCTGGGGAAGACAGATGAGCTCTTCCAGAAAGCGATGAGCACTTGACAG 326
QY 190 cgaataagacggagccgctacgtttaggaattcgttagctcgtggtccag 240
DB 327 CAACAGGGAACACGAGGTGACGCGCCAGAGTACTGTCTCTCTCTCTG 377

RESULT 12
ID T20500 standard; cDNA to mRNA; 488 BP.
AC T20500.
DE 19-JUL-1996 (first entry)
DE Human gene signature HDWG501706.
KM Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
OS cell typing; abnormal cell function; ss.
OS Homo sapiens.
W09514772-81.
PR 01-JUN-1995.
PR 11-NOV-1994; J01916.
PR 12-NOV-1993; JP-355504.
PA (MATSU) MATSUBARA K.
PA (OKUBO) OKUBO K.
PI Matsubara K, Okubo K;
DR WPI; 95-206931/27.
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues
PS Claim 1; Page 652; 2245pp; Japanese.
CC A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in T19001-126837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(I) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.
SQ Sequence 488 BP; 114 A; 99 C; 133 G; 118 T;

Query Match 13.5%; Score 53.4; DB 1; Length 488;
Best Local Similarity 54.1%; Pred. No. 9.8e-07;
Matches 125; Conservative 0; Mismatches 105; Indels 1; Gaps 1;

QY 10 ctggagagcaccctggaggaatcatcaacattccaccagtaactccgttgcggtggg 69
DB 29 CTGGAGAAAGCNCCTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 88
QY 70 catttgaacacctcaacagcgttgatgctgaagcaactatcccaaggaattccaa 129
DB 89 GACAACTTAAGNTCAACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 147
QY 130 aacccctcagaacccaacacacacacacacacacacacacacacacacacacacac 189
DB 148 CTTCTTGGGGAAAGAGACAGATGAGCTCTTCCAGAAAGCGATGAGCACTTGACAG 207
QY 190 cgaataagacggagccgctacgtttaggaattcgttagctcgtggtccag 240
DB 208 CAACAGGGAACACGAGGTGACGCGCGCCAGAGTACTGTCTCTCTCTCTG 258

RESULT 13
ID Q23343 standard; cDNA; 433 BP.
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AC Q23343;
DR 12-AUG-1992 (first entry)
DE Murine Cp-10.
KM Chemotactic protein; neutrophil; monocyte; macrophage;
KW inflammation; autoimmune disease; delayed hypersensitivity;
KW CF; cystic fibrosis; emphysema; diagnosis; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT cds 52..321
FT /tag=a
FT /product=Cp-10

W09204376-A.
PD 19-MAR-1992.
PF 05-SEP-1991; AU0410.
PR 05-SEP-1990; AU-002127.
PR 05-FEB-1991; AU-004463.
PA (HEAR) HEART RES INST LTD.
PI Geczy C, Simpson RJ, Lackmann M;
DR WPI; 92-114301/14.
DR P-PSDB; R22429.
PT New chemotactic protein Cp-10 for altering inflammatory capacity
PT - controls inflammatory conditions, cystic fibrosis and
PT emphysema; antagonists for detecting Cp-10
PS Claim 18; Page 38; 56pp; English.
CC The MCP10 cDNA was derived from a Sepharose-Concanavalin A-activated
CC spleen cell library prep. using cells from A/J mice. Cp-10 has an
CC apparent mol. wt. of ca. 10 kd and is chemotactic for neutrophils,
CC monocytes/macrophages and/or other mammalian cells. Cp-10 is useful
CC (e.g. when admin. locally around a tumour or site of infection) to
CC attract neutrophils etc., esp. in immunocompromised patients or
CC patients allergic to skin test antigens. Antibodies to Cp-10 are
CC useful for control of inflammation and/or tissue damage associated
CC with inflammation, (e.g. due to autoimmune disease or delayed
CC hypersensitivity), cystic fibrosis or emphysema. Ab can also be used
CC to purify Cp-10 and in diagnosis.
SQ Sequence 433 BP; 161 A; 83 C; 87 G; 102 T;

Query Match 13.1%; Score 51.6; DB 1; Length 433;
Best Local Similarity 52.5%; Pred. No. 3.2e-06;
Matches 146; Conservative 0; Mismatches 119; Indels 13; Gaps 1;

QY 3 gactaactgagagaccacttgaggaatcatcaacattccaccagtaactccgttgcg 62
DB 57 GACTGACTGAGAGAGGCGCTTGACGACACCTCATGTGTTCTACCAATTATTCGAAT 116
QY 63 ggttggtgacattcgacacccctcaacaaagcgtgagctgaagcgcgtgatacaaaagg 122
DB 117 ACAGGAAATACACATGCGCTCTACAGATGACTTCAAGAAATGCTCATTCTGAGTG 176
QY 123 ttcccaaacccctcgaagcaccacacacacacacacacacacacacacacacacacac 182
DB 177 TCTCTAGTTTGTGC-----AGAAATATAATTCGAAAACCTGTTCAAGAAAT 223
QY 183 tggatgcgataaagacggagccgctacgtttaggaattcgttagctcgtggtccag 242
DB 224 TGGACATCAATAGTGACATGCAATTAATCTCGAGAGTCTCTCGAGATGATGATAAAG 283
QY 243 tgcgtgaacacgcccacatagatatccacaagaagtag 280
DB 284 TGGGTGTGGCATCTCACAAAGACAGCCACAGAGAGTAG 321

RESULT 14
ID T68321 standard; DNA; 4195 BP.
AC T68321.
DE 16-JUL-1997 (first entry)
DE Human multidrug resistance protein 8 (MRP8) gene.
KM Genetic engineering; MRP; multidrug resistance protein; transgenic;
KW animal model; cell death inhibition; apoptosis; cell proliferation;
KW HIV; human immunodeficiency virus; cancer; cystic fibrosis; neoplasia;
KW tumour; ss.
```


SQ Sequence 10952 BP; 2274 A; 2850 C; 3236 G; 2592 T;

Query Match 10.6%; Score 41.8; DB 1; Length 10952;

Best Local Similarity 61.5%; Pred. No. 0.0087;

Matches 67; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 10 ctggaagaccacttgaggggaatcatcaaatcttccaccagtactccggtcgggtggyg 69

Db 5961 CTGGAGAGGCCCTCGATGTGATGTGCCACCTTCCACAAGTACTCGGCCAAGAGGGT 6020

QY 70 cattcgacacccctcaacaagcgtgagctgaagcagctgatcacaag 118

Db 6021 GACAAGTTCAAGCTCAACAAGTCAGAAAGGAGCTGCTGACCGGG 6069

Search completed: March 14, 2000, 16:18:36
J Time: 1866 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2000, 15:45:30 ; Search time 479.61 Seconds
(without alignments)
3109.583 Million cell updates/sec

Title: US-09-167-705-1
Perfect score: 395
Sequence: 1 atgactaagctggaggaacca.....agcaaaaaaaaaaaaaaa 395

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

ched: 4538634 segs, 1887831982 residues
Total number of hits satisfying chosen parameters: 9077268

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 08
Listing first 45 summaries

Database :

EST.*

1: em_est1:*
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3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
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102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	164.4	41.6	453	43	A1161013
2	164.4	41.6	466	30	AA203475

AA203475 qx55d04.r

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 417)
Miller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, U., Moore, B., Scheilenberg, K., Steptoe, M., Tan, F.,
Thieling, B., White, Y., Wylie, T., Waterson, R. and Wilson, R.
WashU-NCI Human EST Project
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1290672.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@img.lnl.gov) for further information.
Seq primer: -40m3 fwd 5' from Amersham.
Location/Qualifiers
1..417

```

1. 417
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GDB:1335798"
/db_xref="taxon:9606"
/clone_image="436029"
/clone_id="Soares-fetal_liver_spleen_infls_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: Liver and Spleen; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI. This is a subtracted version of the original Soares fetal liver spleen INFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACGCGAGAAATTAATTAAGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

```

Query Match:	40.8%	Score	161.2:	DB	37	Length	417;
Best Local Similarity:	75.5%	Pred	No. 9.6e-35;				
Matches	213;	Conservative	0;	Mismatches	68;	Indels	1;
						Gaps	1;

1	atgactcaagccctggagaccaccctggaggaatcatcaacatcttcacacagtaactccgt	60	
Db	391	ATGACAAAACCTGGAAGACATCTGGAGGGAATTGCATATCTTCCACCAATACTCAGTT	332
Qy	61	cggatgggggcttttcgaacacctcaacaaagctgaagctgaaagagccgatcacaaagga	120
Db	331	CGGAAGGGGCAATTTTGACACCCCTCTTAAAGGTGGGGTGAAGACAGCTGGTTACAA--TGA	273
Qy	121	actcccaaacccctcccgaaacacccaagaagacaaactcactcatgacaaatatccaga	180
Db	272	GCTTCAAAACACATCAAGATATCAAAAGATTAAGCTGTCTATTATGATAAATTTCCAGG	213
Qy	181	cctggaatgcgaataaagaacgagacgctcagctttgaggaatctgaatcctcgtgtccag	240
Db	212	CCTGATGCTATATCAAGATGAAACAGGTGCAGCTTTCAAAGAAATTCATATCCTCGTAGCCAT	153
Qy	241	ggtctgtaaaacagcccatatagatatatccacaagaagcaggt	282
Db	152	TGCGCTGAAGGCTGCCCATTAACACACCCACCAAGAAGTAGGT	111

RESULT
W65311

LOCUS	W65311	439 bp	mRNA	EST	15-OCT-1996
DEFINITION	z333602.r1 Soares fetal_heart.NH9H19W Homo sapiens cDNA clone IMAGE:342458 5' similar to SW:CA6C_PIG P80310 CALGRANULIN C ;, mRNA sequence.				
ACCESSION	W65311				
VERSION	W65311.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
REFERENCE	1 (bases 1 to 439)				
AUTHORS	Hallier,T., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hiltman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,U., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Tevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.				
TITLE	The Mashu-Merck EST Project				
JOURNAL	Unpublished (1995)				
COMMENT	On Apr 14, 1993 this sequence version replaced gi:692790.				

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT On Apr 14, 1993 this sequence version replaced g1:692790.
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LILN ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1367 Std Error: 0.00
 Seq primer: MOD.RGCA+ET.

BASE COUNT	ORIGIN	FEATURES
126 a	105 c	101 g
105 t	2 others	

Query Match	39.28;	Score 155;	DB 26;	Length 439;
Best Local Similarity	76.38;	Pred. No. 5.2e-33;		
Matches 216;	Conservative 0;	Mismatches 65;	Indels 2;	Gaps 2;

Qy	1	atgactaagctcgggagagaccacctgagggaaatctcaaatcttccacccagttactccgt	60
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Qy	61	cgggtcgggcatcttcgacacctcaacaagcgttagctcgaacgacgtcatccacaaggga	120
Db	124	cggaaaggggcattttgacacctctctttaggggttagctgaagcagcttgctttacaa	187
Qy	121	acttcccaaacctctccacacacccaagaagacaaactcttgcatacaaaatattccaga	180
Db	183	gcttccaaacacacatcagaatattcaaaagatgaatgaatgctcattgatgaatattccaa	242
Qy	181	cctgtaatccgataaagccgga-gccctcagcttgtaggaattcgtatgctcctgltcca	238

QY	240	99gfgctgaaacacagccacatatagatatccacaagaagttagt	282
Db	303	TTGGCCCTGAAGGCTGCCATTACCAACACCACCAAGAGTAGGT	345
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LOCUS			
DEFINITION	AA707079	286 bp	mRNA
VERSION	2/28c06.1		EST
KEYWORDS	clone IMAGE:515194 3'		24-DEC-1997
ACCESSION	AA707079		
VERSION	AA707079.1	GI:2716997	
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 286)		
	Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gaisel, G., Jost, S.,		
	Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,		
	Martin, J., Moore, B., Schellenberg, K., Stepec, H., Tan, F.,		
	Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.		
	WashU-NCI human EST project		
	Unpublished (1997)		
COMMENT	On Dec 18, 1997 this sequence version replaced gi:23400250.		

```

Email: est@watson.wustl.edu
This clone is available royalty-free through LINT ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amer sham.
Location/Qualifiers
1..286
FEATURES
source

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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:451594"
/clone_lib="Soares_fetal_liver_spleen_INFLS-S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker. Site.1: Pac I; Site.2: Eco RI.
This is a subcloned version of the original Soares fetal
liver spleen INFLS library. 1st strand cDNA was primed
with a Pac I - Oligo(dT) primer [5'
AATCGAGAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

```

Query Match	38.6%	Score 152.4	DB 37	Length 286
Best Local Similarity	75.2%	Pred. No. 2.4e-32		
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Db	269	ATGACAAACTTGAGAGACATCTGGAGGGAATTGCAATATCTTCACCAATACAGATG	210	
Qy	61	cgagcggggcatttcgacaccctcaacaagcttgagctgaaacagactctatcaagaagga	120	

Db	209	CGGAAGGGGCAATTTTGACACCCCTCTAAAGGTGAGCTGAAGCAGCTGTTACAA- GGA	151
Qy	121	acttcccaaaaacccctccagaacaccaaagaacccaactctatgacaaaatattccaaga	160
Db	150	GCTTGCAAAACCCATCAAGATATCAAAAGATAAAGCTGATGTCATGTCATAATATCCCAAG	91
Qy	181	ccctgattccgataaagaacggaagccgcacagttagaagaattgtagtcctgtrgtccag	240
Db	90	CGTGATGCTTAATCAAGATGAAACAGGTGCACTTTCACGAATTCATCCCTGGTAGCCAT	31
Qy	241	ggtgctgaanaacagccacatagatattcca	270
Db	30	TGCGCTGAAGGCTGCCCCATTGCCACACCA	1

	AA313230	7	RESULT	
LOCUS	AA313230			
DEFINITION	AA313230	311 bp	mRNA	EST
ACCESSION	EE18532	Liver, subcloned (abundant clones)	II Homo sapiens	CDNA
VERSION	AA313230	5' end similar to similar to calgranulin B,		mRNA sequence.
KEYWORDS	AA313230.1	GI:1965761		
SOURCE	EST.			
ORGANISM	human.			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
	Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
REFERENCE	1 (bases 1 to 311)			
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulcher,R.A.,			

Butt,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Cocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wha,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Georgagen,N.S., Glodex,A., Greim,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.T., Marmaros,S.T., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Springs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.R., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

TITLE
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL
Nature 377 (6547 Suppl), 3-174 (1995)

COMMENT
On Apr 18, 1995 this sequence version replaced gi:775522.

Other_ESTs: THC189199
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel.: 3018699056
Fax: 3018699423
Email: arkerlavet@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/cdb/hg1/hg1.html>)
Seq primer: M13 Reverse.

FEATURES	SOURCE
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/db_xref="taxon:9606"	
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/dev_stage="adult"	
note="Organ; liver; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"	
BASE COUNT	93 a 67 c 79 t 2 others
ORIGIN	

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2000, 15:37:00 ; Search time 12.36 Seconds
(without alignments)
95.818 Million cell updates/sec

Title: US-09-167-705-2

Perfect score: 259
Sequence: 1 TKLEPDLEGIINIGHQSVR.....ELKQLGTEKPEPTLQNKKDQ 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 168963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	88.8	92	1 W03563	Calcium binding pr
2	206	79.5	91	1 W01826	Component of bioac
3	206	79.5	91	1 W93819	Angiotropin relate
4	189	73.0	92	1 W03564	Calcium binding pr
5	189	73.0	92	1 W24137	Human chemotacti
6	139	53.7	30	1 R85169	Bovine serum hepar
7	110	42.5	114	1 W17062	Human multitu
8	110	42.5	114	1 W60178	Human calprote
9	83	32.0	91	1 W46607	Human brain protei
10	83	32.0	101	1 R20560	Human mts protei
11	83	32.0	101	1 R80453	Human mts-1 protei
12	74	28.6	66	1 P50052	Sequence of human
13	74	28.6	93	1 W17061	Human multitu
14	74	28.6	93	1 W60177	Human calprote
15	73	28.2	89	1 R22429	Human calprote
16	68	26.3	98	1 W27152	Murine CP-10. New
17	68	26.3	98	1 W82409	Human chemotacti
18	67	25.9	97	1 R26406	Human S100P2 prote
19	67	25.9	97	1 R27058	Sequence of the cl
20	66	25.5	38	1 W46608	Sequence of small
21	58.5	22.6	876	1 W59032	B. pallidus DNA po
22	58.5	22.6	1276	1 W59034	B. pallidus DNA po
23	58	22.4	33	1 W46610	Human brain protei
24	57	22.0	26	1 R49434	Calgranulin B post
25	55	21.2	24	1 R49435	Calgranulin B post
26	55	21.2	3001	1 W19692	ATM mutant 4612del
27	55	21.2	3001	1 W19670	ATM mutant 4612del
28	54.5	21.0	501	1 R27741	Sequence transcrib
29	53	20.5	3722	1 R10145	Cephalosporin anti
30	51.5	19.9	76	1 W75703	Calcium binding pr
31	51.5	19.9	165	1 Y11071	H. pylori ORF 09ge
32	51.5	19.9	213	1 W11072	H. pylori ORF hp2p
33	51.5	19.9	789	1 W14055	Pumpkin ent-kauren
34	50.5	19.5	748	1 W13384	Human protein ubiq

35	50.5	19.5	1084	1 W59033	B. pallidus DNA po
36	50	19.3	208	1 W89231	Mouse osteoprotege
37	50	19.3	401	1 W38344	Mouse osteoprotege
38	50	19.3	540	1 R72678	Protein deduced fr
39	49.5	19.1	120	1 W78465	S. aureus grea prot
40	49.5	19.1	3685	1 P90290	Human Duchenne mus
41	49	18.9	344	1 W98545	H. pylori GHPO 156
42	49	18.9	513	1 W29755	Euphorbia lagascac
43	48.5	18.7	344	1 W20917	H. pylori cell env
44	48.5	18.7	344	1 W53652	H. pylori ORF 14gp
45	48.5	18.7	447	1 W20510	H. pylori inner me

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB ID	Description
1	W03563	88.8	Score 230; DB 1; Best Local Similarity 92.0%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	92	1 W03563	Calcium binding pr
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3	W03563	79.5	Score 206; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	91	1 W93819	Angiotropin relate
4	W03563	73.0	Score 189; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	92	1 W03564	Calcium binding pr
5	W03563	73.0	Score 189; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	92	1 W24137	Human chemotacti
6	W03563	53.7	Score 139; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	30	1 R85169	Bovine serum hepar
7	W03563	42.5	Score 110; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	114	1 W17062	Human multitu
8	W03563	42.5	Score 110; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	114	1 W60178	Human calprote
9	W03563	32.0	Score 83; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	91	1 W46607	Human brain protei
10	W03563	32.0	Score 83; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	101	1 R20560	Human mts protei
11	W03563	32.0	Score 83; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	101	1 R80453	Human mts-1 protei
12	W03563	28.6	Score 74; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	66	1 P50052	Sequence of human
13	W03563	28.6	Score 74; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	93	1 W17061	Human multitu
14	W03563	28.6	Score 74; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	93	1 W60177	Human calprote
15	W03563	28.2	Score 73; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	89	1 R22429	Human calprote
16	W03563	26.3	Score 68; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	98	1 W27152	Murine CP-10. New
17	W03563	26.3	Score 68; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	98	1 W82409	Human chemotacti
18	W03563	25.9	Score 67; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	97	1 R26406	Human S100P2 prote
19	W03563	25.9	Score 67; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	97	1 R27058	Sequence of the cl
20	W03563	25.5	Score 66; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	38	1 W46608	Sequence of small
21	W03563	22.6	Score 58.5; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	876	1 W59032	B. pallidus DNA po
22	W03563	22.6	Score 58.5; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	1276	1 W59034	B. pallidus DNA po
23	W03563	22.4	Score 58; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	33	1 W46610	Human brain protei
24	W03563	22.0	Score 57; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	26	1 R49434	Calgranulin B post
25	W03563	21.2	Score 55; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	24	1 R49435	Calgranulin B post
26	W03563	21.2	Score 55; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	3001	1 W19692	ATM mutant 4612del
27	W03563	21.2	Score 55; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	3001	1 W19670	ATM mutant 4612del
28	W03563	21.0	Score 54.5; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	501	1 R27741	Sequence transcrib
29	W03563	20.5	Score 53; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	3722	1 R10145	Cephalosporin anti
30	W03563	19.9	Score 51.5; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	76	1 W75703	Calcium binding pr
31	W03563	19.9	Score 51.5; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	165	1 Y11071	H. pylori ORF 09ge
32	W03563	19.9	Score 51.5; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	213	1 W11072	H. pylori ORF hp2p
33	W03563	19.9	Score 51.5; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	789	1 W14055	Pumpkin ent-kauren
34	W03563	19.5	Score 50.5; DB 1; Best Local Similarity 88.8%; Pred. NO. 7.7e-26; Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	748	1 W13384	Human protein ubiq

KM angiogenesis; vascular state; mammalian tissue; transfer; cell;
KM genetic information; selective; alteration; nucleic acid content;
KM leukocyte; pig; monocytic-CuRNP.
OS Sue scrofa.
PN DE19628895-A1.
PD 23-JAN-1997.
PF 17-JUL-1996; 028895.
PR 18-AUG-1995; DE-030500.
PR 17-JUL-1995; DE-025992.
PA (FRAU) FRAUNHOFER GES FORDERUNG ANGENANDTEN.
PI Hellmeyer IMG, Kieseletter S, Logemann E, Wissler JH;
DR WPI: 97-088586/09.
DR N-PSDB; T62569.
PT Bioactive metal RNA polypeptide - useful for modulating
PT angiogenesis, etc.
PS Claim 1; Page 15; 16pp; German.
CC A novel bioactive metal RNA polypeptide (RNP) has a RNA component
including the sequence T62568 and a polypeptide component having
the sequence W01826, which is encoded by T62569. The RNP, or
anti-RNP immunoglobulins, can be used to modulate and/or analyse
angiogenesis and the vascular state of mammalian tissue, transfer
genetic information in cells and selectively alter the nucleic
acid content of cells.
CC Leukocytes from pig's blood were cultured in medium, and the
supernatant treated with NH₄ sulphate at 35, 45 and 90% saturation
to precipitate protein fractions. The residual supernatant was
diluted to 45% NH₄ sulphate saturation and concentrated by
ultrafiltration using a 0.5 kD membrane. The retentate was purified
to give 8 mg of product described as monocytic-CuRNP.
SQ Sequence 91 AA;

Query Match 79.5%; Score 206; DB 1; Length 91;
Best Local Similarity 82.0%; Pred. No. 2.1e-22;
Matches 41; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 TKLEDHLEGIINIGHQSVRGHPTLNKYEKOLGTREKPTLQNNKKDQ 50
|||||
Db 1 TKLEDHLEGIINIGHQSVRGHPTLNKYEKOLGTREKPTLQNNKKDQ 50

RESULT 3

ID W93819 standard; peptide; 91 AA.

AC W93819;

DT 21-JUN-1999 (first entry)

DE Angiotropin related protein; ARP; ternary complex; S100 protein;

KM copper-containing ribonucleoprotein; copper; cell selective;

CC morphogenic action; blood capillary endothelial cell; confluent;

CC non-mitogenic induction; cell phenotype; three-dimensional organoid;

KM spatiotemporal supracellular organisation; chemotrophic; blood vessel;

KM tissue neovascularisation; angiogenesis modulation.

OS Synthetic.

PN DE19811047-C1.

PD 15-APR-1999.

PR 13-MAR-1998; 011047.

PR 13-MAR-1998; DE-011047.

PA (FRAU) FRAUNHOFER GES FORDERUNG ANGENANDTEN.

PI Brunner H, Kieseletter S, Koch-Pelster B, Kuhn E;

DR WPI: 99-216114/19.

PT Copper-containing ribonucleoproteins - useful for modulating

PT angiogenesis

PS Disclosure; Page 2; 16pp; German.

CC This invention describes novel copper-containing ribonucleoproteins

CC which are ternary complexes of an S100 protein, copper ions, and

CC RNA comprising the following consensus sequence or its complement

CC GGAAGAUNNNUNNAGUCG1-6CUNNNUNNNNNAAG1-10ANNAACUUNO-5CUNNAGNO-

CC 13AGAA-AUNO-16UAGAG where N = G, A, U or C. The ribonucleoproteins are

CC stated to have the following properties (1) cell-selective morphogenic

CC action in vitro on isolated primary and/or cloned blood capillary

CC endothelial cells in culture for the non-mitogenic induction of the

CC change in cell phenotype from the confluent state, for non-mitogenic

CC alteration of the spatiotemporal supracellular organisation of cells
CC into three-dimensional organoid, capillary-like structures in culture,
CC (2) a specific chemotrophic action on blood vessels in vivo, (3) induction
CC of directional growth of blood vessels in vivo and (4) induction of
CC neovascularisation of tissues through directed ingrowth of blood vessels.
CC Their use for modulating angiogenesis is claimed.
SQ Sequence 91 AA;

Query Match 79.5%; Score 206; DB 1; Length 91;
Best Local Similarity 82.0%; Pred. No. 2.1e-22;
Matches 41; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 TKLEDHLEGIINIGHQSVRGHPTLNKYEKOLGTREKPTLQNNKKDQ 50
|||||
Db 1 TKLEDHLEGIINIGHQSVRGHPTLNKYEKOLGTREKPTLQNNKKDQ 50

RESULT 4

ID W03564 standard; Protein; 92 AA.

AC W03564;

DT 01-MAY-1997 (first entry)

DE Calcium binding protein CAAFI.

KM Calcium binding protein; human; amniotic fluid; S100 protein family;

KM intracellular signal transduction; squamous epithelial cell; neutrophil;

KM macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;

KM squamous cell carcinoma; skin; oesophagus; CAAFI; lung; blood disease.

OS Homo sapiens.

PN EP-731166-A2.

PD 11-SEP-1996.

PE 04-DEC-1995; 119045.

PR 06-MAR-1995; JP-070468.

PR 06-MAR-1995; JP-045564.

PA (HITO/) HITOMI J.

PA (TOFU) TONEN CORP.

PI Hitomi J, Kimura T, Yamaguchi K, Yamamura T;

DR WPI: 96-403989/41.

DR N-PSDB; T39346.

PT New human or bovine calcium binding protein and related nucleic acid

PT - is a marker for inflammation, neoplasia, skin and blood diseases

PS Claim 1; Page 24; 36pp; English.

CC This sequence represents the CAAFI calcium-binding protein isolated from

CC human amniotic fluid. CAAFI belongs to the S100 protein family, which

CC includes calyculin, MRP8, and MRP14. Intracellular calcium ion

CC concentration is one of the key factors for intracellular signal

CC transduction. The calcium signals are transduced by various

CC calcium-binding proteins, such as this protein. CAAFI is normally

CC expressed in squamous epithelial cells, neutrophils and macrophages, but

CC atypical epithelial cells are negative for CAAFI and overexpression is

CC observed in several types of cancer cells and neutrophils/macrophages

CC infiltrating cancerous lesions. Detection of CAAFI (using antibodies in

CC usual immunoassays) can be used to diagnose (or monitor) inflammation,

CC neoplasia (particularly squamous cell carcinoma of the skin, oesophagus,

CC lung and cervix), and skin and blood diseases.

SQ Sequence 92 AA;

Query Match 73.0%; Score 189; DB 1; Length 92;
Best Local Similarity 74.0%; Pred. No. 5.7e-20;
Matches 37; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 TKLEDHLEGIINIGHQSVRGHPTLNKYEKOLGTREKPTLQNNKKDQ 50
|||||
Db 2 TKLEDHLEGIINIGHQSVRGHPTLNKYEKOLGTREKPTLQNNKKDQ 51

RESULT 5

ID W24137 standard; Protein; 92 AA.

AC W24137;

DT 28-JAN-1998 (first entry)

DE Human chemotactic cytokine I.

1 >

1

CC bladder, grow and become symptomatic. Struvite stones (MgNH₄PO₄) are
CC commonly found after urinary tract infection. The mechanisms of this and
CC other stone formation is unclear, but some urine compositions are known
CC to inhibit formation. One of the major components of these is a protein
CC factor calprotectin, which inhibits mineral precipitation. Calprotectin
CC can also be used to raise antibodies, which in turn can be used to detect
CC the protein in samples. The levels of calprotectin found in samples can
CC be compared to levels found in normal humans, and thus assuming increased
CC calprotectin correlates to indication of kidney stone formation, this
CC procedure can be used as a diagnostic tool.
SQ Sequence 114 AA;

Query Match 42.5%; Score 110; DB 1; Length 114;
Best Local Similarity 51.1%; Pred. No. 1.6e-08;
Matches 23; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 TRKEDHLEGINIGHOYSVRVGHFDLTKKELQGLTKELPKLQ 45
DB 6 SQERNETIRITFHQYSVRLGHFDLTKKELQGLTKELPKLQ 50

W46607
ID W46607 standard; protein; 91 AA.
AC W46607;
DT 01-JUL-1998 (first entry)
DE Human brain protein S100b beta subunit.
KW Human brain protein S100b; cerebral; neural; antibody;
KW Immunological assay; diagnosis; cerebral dysfunction;
KW Melanoma cancer.
OS Homo sapiens.
PN WO9801471-A1.
PD 15-JAN-1998.
PF 27-JUN-1997; SE1164.
PR 05-JUL-1996; SF-002677.
PA (SANG-) SANGTEC MEDICAL AB.
PI Brundell J, Nyberg L;
DR WPI; 98-100999/09.
PT Peptide(s) from human brain protein S100b beta fragments useful in
PT S100 assay - by producing antibodies directed to the peptide(s),
PT useful e.g. for diagnosis and monitoring of cerebral dysfunction and
PT melanoma cancer.
PS Disclosure; Page 18-19; 29pp; English.
CC The Human brain protein S100b is known to be one of a number of soluble
CC small molecule weight proteins which are released into the cerebral
CC extracellular fluid due to cellular disruption of nervous tissue and
CC cells of neural origin. The beta subunit of the protein has been used
CC to produce epitopes (W46608-W46614) and corresponding antibodies which
CC can be used in immunological assay methods. Determining the presence of
CC brain protein S100b allows diagnosis and monitoring of patients with
CC cerebral dysfunction and melanoma cancer.
SQ Sequence 91 AA;

Query Match 32.0%; Score 83; DB 1; Length 91;
Best Local Similarity 40.0%; Pred. No. 8.6e-05;
Matches 20; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

QY 1 TRKEDHLEGINIGHOYSVRVGHFDLTKKELQGLTKELPKLQ 50
DB 1 SELEKAVVALIDVHFQYSGREGDKHKLKSELKELINNELSHLEIKQ 50

RESULT 10
R20560
ID R20560 standard; protein; 101 AA.
AC R20560;
DT 14-MAY-1992 (first entry)
DE Human mts protein.
KW Metastatic cancer; antibodies; mouse; lung; liver; kidney; thyroid;
KW Breast cancer; cell growth.
OS Homo sapiens.

FH Key Location/Qualifiers
FT protein 1..101
FT /label= mts-1
FT peptide 2..11
FT /note= "antigenic"
FT peptide 22..37
FT /note= "antigenic; calcium binding domain"
FT peptide 42..54
FT /note= "antigenic"
FT peptide 87..101
FT /note= "antigenic"

PN WO9200757-A.
PD 23-JAN-1992.
PF 09-JUL-1991; U04832.
PR 09-JUL-1990; US-550600.
PA (RESE) RES CORP TECHN INC.
PI Zain S, Lukanidin E;
DR WPI; 92-056647/07.
DR N-PSDB; Q20506.
PT Metastatic cancer diagnosis by detection of mts-1 gene or protein
PT - using antibody treatment of cancer and tumours of e.g. kidney,
PT thyroid, lung and liver
PS Claim 9; Fig 2; 82pp; English.
CC The sequence was deduced from the DNA sequence obtd. by screening a
CC human cDNA library with mouse mts-1 cDNA probes. The antigenic
CC mts-1 peptides (see features) derived from the protein and anti-
CC bodies raised to them are useful in the diagnosis of metastatic
CC cancer, e.g. lung, kidney, thyroid or breast cancer. The peptide
CC comprising the calcium binding site generates antibodies reactive
CC with many members of the calcium binding protein family; the other
CC three peptides are unique to mts-1 and generate antibodies specific
CC only for this protein. Cell lines capable of expressing mts-1 are
CC useful as model systems for in vitro and in vivo anti-metastasis
CC drug screening. Pharmaceutical compns. contg. the mts-1 protein or
CC anti-cancer reagents may be used to promote cell growth, or for
CC treating cancer, respectively.
SQ Sequence 101 AA;

Query Match 32.0%; Score 83; DB 1; Length 101;
Best Local Similarity 41.7%; Pred. No. 9.8e-05;
Matches 20; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 3 LEDHLEGINIGHOYSVRVGHFDLTKKELQGLTKELPKLQ 50
DB 5 LKRALDVWVSTFHKYSKRGDKFKLKLKSELKELRLRELPFGKRTPE 52

RESULT 11
R80453
ID R80453 standard; protein; 101 AA.
AC R80453;
DT 27-DEC-1995 (first entry)
DE Human mts-1 protein.
KW Metastasis; cancer; mts-1 gene; tumour; therapy.
OS Homo sapiens.
PN WO9520656-A1.
PD 03-AUG-1995.
PF 31-JAN-1995; U01214.
PR 31-JAN-1994; US-190560.
PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
PI Lukanidin E, Zain S;
DR WPI; 95-275441/36.
DR N-PSDB; Q99177.
PT Nucleic acid encoding human mts-1, antigenic fragments and
PT antibodies - useful for diagnosis of malignant cancer and metastatic
PT potential of tumour cells.
PS Claim 12; Page 92; 124pp; English.
CC A human cDNA library was constructed in lambda-gt10 using poly(A)+
CC RNA prepd. from HeLa cells. The library was screened with a 32p-
CC labeled mouse mts-1 vDNA probe. A clone was obtd. which comprised
CC the full-length human mts-1 gene. The encoded protein is used for
CC the diagnosis or therapy of cancer, and to raise antibodies.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 14, 2000, 15:37:00 ; Search time 13.75 Seconds
(without alignments)
171.525 Million cell updates/sec

Title: US-09-167-705-2

Perfect score: 259
Sequence: 1 TKLEDEHLEGIINIGHQYVSR.....ELKQLGTEKLPKTKNQXKQ 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Sched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR62:*

1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	79.5	91	2	A55406
2	189	73.0	92	2	JC4712
3	131	50.6	122	1	A42628
4	114	44.0	113	1	JN0686
5	110	42.5	114	1	B31848
6	89	34.4	101	2	S06207
7	87	33.6	95	2	S24146
8	87	33.6	101	2	S01759
9	84	32.4	92	1	BCHURB
10	84	32.4	92	1	A26557
11	84	32.4	92	2	A48015
12	83	32.0	91	1	BCB01B
13	83	32.0	100	2	A53217
14	83	32.0	101	2	A48219
15	81	31.3	591	2	A45135
16	78	30.1	113	1	S68242
17	77	29.7	306	1	A48118
18	74	28.2	93	1	BCHUCF
19	73	28.2	89	1	I56163
20	72	27.8	95	1	S35985
21	71	27.4	94	1	BCHURA
22	71	27.4	94	1	BCB01A
23	70	27.0	89	1	JN0685
24	69.5	26.8	110	2	B48219
25	68	26.3	90	1	BCHUY
26	68	26.3	98	2	JC5064
27	68	26.3	98	2	JC5065
28	67	25.9	90	1	S27011
29	67	25.9	98	2	A41988
30	65	25.1	217	2	J50330

31	64	24.7	89	2	A54314	calcyclin - mouse
32	64	24.7	90	2	B28363	calcyclin - rat
33	63	24.3	102	1	J01300	calgizarin - rabb
34	61	23.6	97	2	A30129	S-100 protein, lun
35	61	23.6	469	2	S55167	IME2-dependent sig
36	60.5	23.4	97	1	JH0663	calpactin I light
37	60.5	23.4	438	2	H72241	fixc protein - The
38	58.5	22.6	97	2	A28489	calpactin I light
39	57.5	22.2	2108	2	S28417	COG39 protein - ye
40	57	22.0	41	2	B42628	calcium-binding pr
41	56.5	21.8	95	1	LDG10	calpactin I light
42	56.5	21.8	97	2	JC1139	calpactin I light
43	56.5	21.8	97	2	B28489	calpactin I light
44	56.5	21.8	416	1	G64424	histidine--tRNA li
45	56	21.6	105	1	I37080	calgizarin - huma

ALIGNMENTS

RESULT 1
A55406
calgranulin C - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 23-May-1997
C:Accession: A55406
R:Del/Insert: A.C.; Schleicher, C.H.; Santome, J.A.
J. Biol. Chem. 269, 28929-28936, 1994
A:Title: Primary structure and binding properties of calgranulin C, a novel S100-like
A:Reference number: A55406; MUID:95050708
A:Accession: A55406
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-91
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; EF hand
F:48-80/Domain: calmodulin repeat homology <EF2>

Query Match 79.5% Score 206; DB 2; Length 91;
Best Local Similarity 82.0% Pred. No. 6e-19;
Matches 41; Conservative 3; Mismatches 6; Gaps 0;
Oy 1 TKLEDEHLEGIINIGHQYVSRGHFTLNKYELEKQLGTEKLPKTKNQXKQ 50
Db 1 TKLEDEHLEGIINIGHQYVSRGHFTLNKYELEKQLGTEKLPKTKNQXKQ 50
RESULT 2
JC4712
S-100 calcium-binding protein A12 - human
N:Alternate names: calcium-binding amniotic fluid protein 1 (CAAF1); calgranulin C; c
utrophin protein
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence_revision 19-Jun-1996 #text_change 13-Aug-1999
C:Accession: JC4712; JC4717; JC4891; S56113; S56114
R:Yamamura, T.; Hitomi, J.; Nagasaki, K.; Suzuki, M.; Takahashi, E.; Saito, S.; Tsuka
Biochem. Biophys. Res. Commun. 221, 356-360, 1996
A:Title: Human CAAF1 gene - molecular cloning, gene structure, and chromosome mapping
A:Reference number: JC4712; MUID:96192053
A:Accession: JC4712
A:Molecule type: mRNA
A:Residues: 1-92 <YAN>
A:Cross-references: DDBJ:D83657; NID:G1502284; PIDN:BAAL2030.1; PID:G1502285
R:Matli, T.; Ertmann, K.D.; Gallin, M.Y.
Biochem. Biophys. Res. Commun. 221, 454-458, 1996
A:Title: Host-parasite interaction in human onchocerciasis: Identification and sequen
A:Reference number: JC4717; MUID:96192069
A:Accession: JC4717
A:Molecule type: protein
A:Residues: 2-92 <MAR>
A:Experimental source: Onchocerca volvulus infecting human tissue
R:Ilg, E.C.; Troxler, H.; Buegisser, D.M.; Kuster, T.; Markert, M.; Gulgnard, F.; Hu

Blochem. Biophys. Res. Commun. 225, 146-150, 1996
 A.Title: Amino acid sequence determination of human S100 A12 (P6, Calgranulin C, CGRP, C
 A.Reference number: J04891; MUID:96332419
 A.Accession: J04891
 A.Molecule type: protein
 A.Residues: 2-92 <ILG>
 R:Guignard, F.; Manuel, J.; Markert, M.
 Blochem. J. 309, 395-401, 1995
 A.Title: Identification and characterization of a novel human neutrophil protein related
 A.Reference number: S56113; MUID:9351965
 A.Accession: S56113
 A.Status: preliminary
 A.Molecule type: protein
 A.Residues: 'xx', 4-14, 'X', 16-17, 'xxxx' <GUII>
 A.Experimental source: Isoform 6a
 A.Accession: S56114
 A.Status: preliminary
 A.Molecule type: protein
 A.Residues: 2-21 <GUI2>
 A.Experimental source: Isoform 6b
 Comment: This protein is released by activated neutrophils in the course of inflammato
 nnelis:
 Gene: GDB:S100A12; p6; MRP6; CGRP; CAAP1
 A.Cross-references: GDB:5218374
 A.Map position: 1q21-1q21
 C-Complex: monomer
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: calcium binding; EF hand; monomer; neutrophil; zinc
 F:2-92/Product: S-100 calcium-binding protein A12 #status experimental <MAT>
 F:6-39/Domain: calmodulin repeat homology <EFI>
 F:49-81/Domain: calmodulin repeat homology <EFI>
 F:86-90/Region: zinc binding #status predicted

```

Query Match 73.0% Score 189; DB 2; Length 92;
Best Local Similarity 74.0%; Pred. No. 8e-17;
Matches 37; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 TLKLEHLEGIINIGHQSVRVGHFDTLNKLYELKQGTGFKELPFTLONXKQ 50
|||||-----||| ||||| ||||| ||||| ||||| |||
DB 2 TLKEHLEGIIVNFHQSYSRKGHFDTLSKGLKQLTTELANTINKINDK 51

RESULT 3
A42628
calgranulin B - bovine (fragment)
N1: Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory factor
in 2
C:Species: Bos primigenius taurus (cattle)
Accession: B22309 #sequence_revision 23-May-1997 #text_change 23-May-1997
Submitter: T.K.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Chen,
submitted to the Protein Sequence Database, July 1992
A:Reference number: A22309
A:Accession: B22309
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-122 <TAN>
R:Dianoux, A.C.; Sasas, M.J.; Garin, J.; Gagnon, J.; Vignals, P.V.
Biochemistry 31, 5898-5905, 1992
A:Title: The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutrophils
A:Reference number: A42628; MUID:92304974
A:Accession: A42628
A:Molecule type: protein
A:Residues: 4-32, 'F', 34-56 <DIA>
C:Complex: heterodimer and higher complexes with calgranulin A
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; phospho-
F:50-82/Domain: calmodulin repeat homology <EF2>
Query Match 50.6% Score 131; DB 1; Length 122;

```

```

Qy      1 TLEDDLEGINIGHQYRVGHPDITLNLKYLKQIGTKEPLKTXK 48
      ::: : : : : : : : : : : : : : : : : : : : : : : : :
Db      2 SOMESEITFINIFHQYRVGLGHYITLLQKEKQVLQVQKELPPLFKK 49

Best Local Similarity 56.2%; Pred. No. 1.9e+09;
Matches 27; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

```

RESULT 4

JN0686

calgranulin B - rat

N:Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory fa

C:Species: Rattus norvegicus (Norway rat)

C:Date: 03-May-1994 #sequence.revision 23-May-1997 #text_change 22-Jun-1999

C:Accession: JN0686

R:Imamichi, T.; Uchida, I.; Wahl, S.M.; McCartney-Francis, N.

Biochem. Biophys. Res. Commun. 194, 819-825, 1993

A:Title: Expression and cloning of migration inhibitory factor-related protein (MRP)8

A:Reference number: JN0685; MUID:93343942

A:Accession: JN0686

A:Molecule type: mRNA

A:Residues: 1-113 <IMA>

A:Cross-references: GB:LI8948; NID:g488156; PIDN:AAA18214.1; PID:g488157

C:Genetics:

A:Gene: MRP14

C:Complex: heterodimer and higher complexes with calgranulin A

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: acetylated amino end; calcium binding; EF hand; heterodimer; inflammation

F:1-113/Product: calgranulin B #status predicted <MAT>

F:1-145/Domain: calmodulin repeat homology <EP1>

F:55-87/Domain: calmodulin repeat homology <EP2>

F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

F:80-91/Disulfide bonds: #status predicted

RESULT 5

B31848

calgranulin B - human

N.Alternate names: calcium-binding protein MRP-14; cystic fibrosis-associated antigen (MRP-14); MIF-related 14k protein; S-100 calcium-binding protein A9 (S100A9)

C.Species: Homo sapiens (man)

C.Date: 21-May-1990 #sequence-revision 23-May-1997 #text-change 22-Jun-1999

C.Accession: B31848; S00667; A33819; B60911; B61082; D54327

R.Lagasse, E.; Clerc, R.G.

Mol. Cell. Biol. 8, 2402-2410, 1988

A.Title: Cloning and expression of two human genes encoding calcium-binding proteins

A.Reference number: A93102; MUID:88302148

A.Accession: B31848

A.Molecule type: DNA

A.Residues: 1-114 <LAG>

A.Cross-references: GB:K21064; NID:g188669; PIDN:AAA36326.1; PID:g386958

R.Odink, K.; Cerletti, N.; Brueggen, J.; Clerc, R.G.; Tarscay, L.; Zwadlo, G.; Gerhar

Nature 330, 80-82, 1987

A.Title: Two calcium-binding proteins in infiltrate macrophages of rheumatoid arthritis

A.Reference number: S00667; MUID:88039099

A.Accession: S00667

A.Molecule type: mRNA

A.Residues: 1-114 <ODIC>

A.Cross-references: EMBL:X06233; NID:g34770; PIDN:CAA29579.1; PID:g34771

A.Note: parts of this sequence were confirmed by protein sequencing

R.Murao, S.; Collart, F.R.; Huberman, E.

J. Biol. Chem. 264, 8356-8360, 1989

A.Title: A protein containing the cystic fibrosis antigen is an inhibitor of protein

A.Reference number: A33819; MUID:89255276

Gene 87, 219-223, 1990

A:Title: Structure of gene mtsl, transcribed in metastatic mouse tumor cells.

A:Reference number: JH0097; MUID:90236313

A:Accession: JH0097

A:Molecule type: DNA

A:Residues: 1-101 <TUI>

A:CROSS-references: GB:M36578; GB:M36579

R:Experimental source: liver

R:TULCHINSKY, B.

submitted to the EMBL Data Library, August 1989

A:Reference number: S07981

A:Accession: S07981

A:Molecule type: DNA

A:Residues: 1-47,'VSSGXFXNG','56-57','RTDEA' <TU2>

A:CROSS-references: EMBL:X16094; NID:g53249; PIDN:CAA34224.1; PID:g53250

R:Jackson-Grusby, L.L.; Swiergiel, J.; Linzer, D.I.H.

Nucleic Acids Res. 15, 6677-6690, 1987

A:Title: A growth-related mRNA in cultured mouse cells encodes a placental calcium bl

A:Reference number: A26803; MUID:67316927

A:Accession: A26803

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-101 <GOT>

A:CROSS-references: GB:XO5835; NID:g50310; PIDN:CAA29282.1; PID:g50311

J. Biochem. 103, 48-53, 1988

R:Goico, K.; Endo, H.; Fujiyoshi, T.

A:Title: Cloning of the sequences expressed abundantly in established cell lines: Ide

A:Reference number: A41411; MUID:88198109

A:Accession: A41411

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-101 <GOR>

A:CROSS-references: GB:D00208; NID:g220569; PIDN:BAA00148.1; PID:d1000593; PID:g22057

R:Tulichnsky, E.; Krimerov, D.; Ford, H.L.; Reshetnyak, E.; Lukandin, E.; Zain, S.

Oncogene 8, 79-86, 1993

A:Title: Characterization of a positive regulatory element in the mtsl gene.

A:Reference number: I48674; MUID:93141279

A:Accession: I48674

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-47,'VSGSXFXNGQ','48-54' <RES>

A:CROSS-references: EMBL:X16094; NID:g53249; PIDN:CAA34224.1; PID:g53250

C:Comment: Gene mtsl is expressed in metastatic cells.

C:Genetics:

A:Gene: mtsl

A:introns: 47/3

C:Superfamily: S-100 protein; calmodulin repeat homology

C:keywords: calcium binding; cancer; EF hand

F:7/41/Domain: calmodulin repeat homology <EF1>

F:50-82/Domain: calmodulin repeat homology <EF2>


```

QY      1  TKLEDDHEGIIINIGHQYSVRVGHFDTLNKRYELKQLGTEKPLRTIIONKQD 50
        ::::  :||:  ||||  |  |  ||||  ||  |  :||:  ||
Db      2  SELEKAWALLIDVPHQYSGREGDKHKLKSELSKETINNELSHPLEEIKEQ 51
        :||:  :||:  ||||  |  |  ||||  ||  |  :||:  ||

RESULT  12
BCBOIB
S-100 protein beta chain - bovine
N:Alternate names: neurocalcin delta-binding protein S100-beta
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-May-1979 #sequence.revision 14-Nov-1983 #text-change 07-May-1999
C:Accession: A91254; B91110; A90075; S54348; A03077
R:Isobe, T.; Okuyama, T.
Eur. J. Biochem. 89, 379-388, 1978
A:Title: The amino-acid sequence of S-100 protein (PAP-I-b protein) and its relation
A:Reference number: A91254; MUID:79045265
A:Accession: A91254
A:Molecule type: protein
A:Residues: ESEL, 5-91 <ISO>
A:Experimental source: brain
A:Note: this sequence has since been revised in reference A91110
R:Isobe, T.; Okuyama, T.
Eur. J. Biochem. 116, 79-86, 1981
A:Title: The amino-acid sequence of the alpha subunit in bovine brain S-100 a protein
A:Reference number: A91110; MUID:81236562
A:Accession: B91110
A:Molecule type: protein
A:Residues: 1-91 <IS2>
R:Baudier, J.; Gerard, D.
Biochemistry 22, 3360-3369, 1983
A:Title: Ions binding to S100 proteins: structural changes induced by calcium and zinc
A:Reference number: A90471; MUID:8400339
A:Contents: annotation; metal ion-binding properties
R:Marshall, D.R.; Umekawa, H.; Waterson, D.M.; Hidaka, H.
Arch. Biochem. Biophys. 240, 777-780, 1985
A:Title: Structural characterization of the calcium binding protein S100 from adipose
A:Reference number: A90075; MUID:65278169
A:Accession: A90075
A:Molecule type: protein
A:Residues: 1-91 <MAR>
C:Experimental source: adipose tissue
R:Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
Biochem. J. 306, 551-555, 1995
A:Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in g
A:Reference number: S54343; MUID:95194333
A:Accession: S54348
A:Molecule type: protein
A:Residues: 56-61, 'N', 63-79, 'V' <OKA>
A:Comment: The S-100 protein is composed of two related polypeptide chains, alpha and
brain proteins. S-100 is also found in a variety of other tissues.
C:Comment: S-100 is an intracellular protein that weakly binds calcium. It binds zinc
cium-binding sites.
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: brain; calcium binding; EF hand; zinc
F:5-39/Domain: calmodulin repeat homology <EF1>
F:48-80/Domain: calmodulin repeat homology <EF2>
F:1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental
F:18,21,23,26,31/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
F:61,63,65,67,72/Binding site: calcium (Asp, Asp, Glu, Glu) #status predicted

Query Match 32.0%: Score 83; DB 1; Length 91;
Best Local Similarity 40.0%: Pred. No. 0.0013;
Matches 20; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

1  TKLEDDHEGIIINIGHQYSVRVGHFDTLNKRYELKQLGTEKPLRTIIONKQD 50

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S112_PIG STANDARD; PRT; 91 AA.
 ID S112_PIG
 AC P80310;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CALGRANULIN C (CAGC).
 GN S100A12.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-GRANULOCYTE;
 RX MEDLINE: 95050708.
 RA DELL'ANGELO E.C., SCHLEICHER C.H., SANTOME J.A.;
 RT "Primary structure and binding properties of calgranulin C, a novel
 RT S100-like calcium-binding protein from pig granulocytes.";
 RL J. Biol. Chem. 269:28929-28936(1994)
 CC -1- TISSUE SPECIFICITY: FOUND ESSENTIALLY IN GRANULOCYTES WITH SMALL
 CC AMOUNTS FOUND IN LYMPHOCYTES.
 CC -1- MISCELLANEOUS: IN THE ABSENCE OF ZINC BINDS ONE CALCIUM ION PER
 CC MOLECULE, IN THE PRESENCE OF ZINC BINDS TWO CALCIUM IONS PER
 CC MOLECULE.
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
 CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
 DR HSSP: P02632; ICB1.
 DR PROSITE: PS00018; EF_HAND; FALSE_NEG.
 DR PROSITE: PS00303; S100_CABP; 1.
 DR PFAM: PF00036; efhand; 1.
 DR PFAM: PF01023; S_100; 1.
 KW Calcium-binding; zinc; Metal-binding.
 FT CA_BIND 18 31 SITE I (LOW AFFINITY) (BY SIMILARITY).
 FT CA_BIND 61 72 SITE II (HIGH AFFINITY) (BY SIMILARITY).
 SQ SEQUENCE 91 AA; 10614 MM; DB5F6EF CRC32;
 QY 1 TKLEHLEGIINIGHOYSVRGHFDLTKYELKQLGTKEPKTLXKKDQ 50
 DB 1 TKLEHLEGIINIGHOYSVRGHFDLTKYELKQLGTKEPKTLXKKDQ 50
 RESULT 3
 S112_HUMAN STANDARD; PRT; 91 AA.
 ID S112_HUMAN
 AC P80511;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CALGRANULIN C (CAGC) (P6) (CGRP) (NEUROPHIL S100 PROTEIN) (CALCIUM-
 DE BINDING PROTEIN IN AMNIOTIC FLUID 1) (CAAF1).
 GN S100A12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97138564.
 RA WICKI R., NARENHOLZ I., MISCHKE D., SCHAEFER B.W., HEIZMANN C.W.;
 RT "Characterization of the human S100A12 (calgranulin C, p6, CAAF1,
 RT CGRP) gene, a new member of the S100 gene cluster on chromosome
 RT 12p21.";
 RL Cell Calcium 20:459-464(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96192053.
 RA YAMAMURA T., HITOMI J., NAGASAKI K., SUZUKI M., TAKAHASHI E.,
 RA SAITO S., TSUKADA T., YAMAGUCHI K.;
 RT "Human CAAF1 gene -- molecular cloning, gene structure, and chromosome

RT mapping.";
 RL Biochem. Biophys. Res. Commun. 221:356-360(1996).
 RN [3]
 RP SEQUENCE.
 RX MEDLINE: 96192069.
 RA MARTI T., ERTTMANN K.D., GALLIN M.Y.;
 RT "Host-parasite interaction in human onchocerciasis: Identification
 RT and sequence analysis of a novel human calgranulin.";
 RL Biochem. Biophys. Res. Commun. 221:454-458(1996).
 RN [4]
 RP SEQUENCE.
 RC TISSUE-NEUTROPHILS;
 RX MEDLINE: 96332419.
 RA IUG E.C., TROXLER H., BUEGESSER D.M., KOSTER T., MARKERT M.,
 RA GUIGNARD F., HUNZIKER P., BIRCHLER N., HEIZMANN C.W.;
 RT "Amino acid sequence determination of human S100A12 (p6, calgranulin
 RT C, CGRP, CAAF1) by tandem mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 225:146-150(1996).
 RN [5]
 RP SEQUENCE OF 1-20.
 RX MEDLINE: 95351965.
 RA GUIGNARD F., MAUEL J., MARKERT M.;
 RT "Identification and characterization of a novel human neutrophil
 RT protein related to the S100 family.";
 RL Biochem. J. 309:395-401(1995).
 CC -1- SUBUNIT: MONOMER.
 CC -1- TISSUE SPECIFICITY: MONOCYTES AND LYMPHOCYTES.
 CC -1- MASS SPECTROMETRY: MW=10444; METHOD-ELECTROSPRAY.
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
 CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: X97859; CAA66453.1; -
 DR EMBL: X98288; CAA66934.1; -
 DR EMBL: X98289; CAA66934.1; JOINED.
 DR EMBL: X98290; CAA66934.1; JOINED.
 DR EMBL: D49549; BAA08497.1; -
 DR EMBL: D83664; BAA12036.1; -
 DR EMBL: D83657; BAA12030.1; -
 DR HSSP: P02633; 1BOD.
 DR MTM: 603112; -
 DR PROSITE: PS00018; EF_HAND; FALSE_NEG.
 DR PROSITE: PS00303; S100_CABP; 1.
 DR PFAM: PF00036; efhand; 1.
 DR PFAM: PF01023; S_100; 1.
 KW Calcium-binding; zinc; Metal-binding.
 FT INIT_MET 0
 FT CA_BIND 18 31 SITE I (LOW AFFINITY) (BY SIMILARITY).
 FT CA_BIND 61 72 SITE II (HIGH AFFINITY) (BY SIMILARITY).
 SQ SEQUENCE 91 AA; 10444 MM; E91A6B59 CRC32;
 QY 1 TKLEHLEGIINIGHOYSVRGHFDLTKYELKQLGTKEPKTLXKKDQ 50
 DB 1 TKLEHLEGIINIGHOYSVRGHFDLTKYELKQLGTKEPKTLXKKDQ 50
 RESULT 4
 S112_RABIT STANDARD; PRT; 81 AA.
 ID S112_RABIT
 AC 077791;
 DT 15-JUL-1999 (Rel. 38, Created)

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DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CALGRANULIN C (CAGC) (FRAGMENT).
GN S100A12.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=NEUTROPHILS;
RX MEDLINE; 96355278.
RA YANG Z., DEVERER M.J., GARDINER E.E., DEVENISH R.J., HANDLEY C.J.,
RA UNDERWOOD J.R., ROBINSON H.C.;
RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
RT calgranulin C when incubated with inorganic [35S]sulfate.";
RL J. Biol. Chem. 271:19802-19809(1996).
CC 1-1. SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
CC -----
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CC -----
DR EMBL; AF091848; AAC61770.1; .
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
DR PFAM; PF00036; efhand; 1.
DR PFAM; PF01023; S_100; 1.
RW Calcium-binding.
FT NON_TER 1 1
FT CA_BIND 8 21
FT CA_BIND 51 62
SO SEQUENCE 81 AA; 9401 MW; 4AE11912 CNC32;

Query Match 52.5%; Score 136; DB 1; Length 81;
Best Local Similarity 67.5%; Pred. No. 6.7e-11;
Matches 27; Conservative 5; Mismatches 8; Incls 0; Gaps 0;

QY 11 INIGHQYSVRVGHFDLTNKLKELKQGLKELPKLTQNKXKQ 50
   ||||||| :|:|:|:| |||:| ||| :|:| |||
Db 1 INIFHQYSVRGHYDLSKCELKLTTELVTYIKTKRQ 40

S100A12
S100A12_BOVIN STANDARD; PRT; 122 AA.
ID S109_BOVIN
AC P28783;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CALGRANULIN B (NEUTROPHIL CYTOSOLIC 23 KD PROTEIN) (P23) (BEE22)
DE (FRAGMENT).
DE S100A9.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE.
RC TISSUE=ESOPHAGEAL EPITHELIUM;
RX MEDLINE; 93280230.
RA TANG T.K., HONG T.-M., LIN C.-Y., LAI M.-L., LIU C.H.L., LO H.-J.,
RA WANG M.-E., CHEN L.B., CHEN W.-T., IP W., LIN D.C., LIN J.J.-C.,
RA LIN S., SUN T.-T., WANG E., WANG J.L., WU R., WU C.-W., CHEN S.;
RT "Nuclear proteins of the bovine esophageal epithelium. I. Monoclonal
RT antibody W2 specifically reacts with condensed nuclear of
RT differentiated superficial cells.";
RL J. Cell Sci 104:237-247(1993).
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RN      [2]          SEQUENCE OF 4-56.
RP      TISSUE-NEUTROPHILS;
RX      MEDLINE: 92304974.
RA      DINOIX A.-C., STASIA M.-J., GARIN J., GAGNON J., VIGNAIS P.V.;
RT      "The 23-kilodalton protein, a substrate of protein kinase C, in
RL      bovine neutrophil cytosol is a member of the S100 family.";
CC      Biochemistry 31:5898-5905(1992).
CC      -1 SUBUNIT: DISULFIDE LINKED HETERODIMER OF A 7/11 KD AND A 22/23 KD
CC      SUBUNITS.
CC      -1 SUBCELLULAR LOCATION: CYTOPLASMIC; LOOSELY ASSOCIATED TO THE
CC      CYTOSKELETON.
CC      -1 TISSUE SPECIFICITY: FOUND ESSENTIALLY IN PHAGOCYtic CELLS.
CC      -1 PMR: PHOSPHORYLATED BY PROTEIN KINASE C.
CC      -1 MISCELLANEOUS: CONTAINS TWO CA(2+)-BINDING DOMAINS PER PROTEIN.
CC      -1 SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
CC      MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
DR      HSSP: P02638; ICFF.
DR      PROSITE, PS00018; EF_HAND. PARTIAL.
DR      PROSITE, PS00303; S100_CABP; 1.
DR      PFAM; PF01023; ehand; 1.
FT      CA_BIND 19 32 SITE I (LOW AFFINITY) (POTENTIAL).
FT      CA_BIND 53 64 SITE II (HIGH AFFINITY) (POTENTIAL).
SQ      SEQUENCE 122 AA; 13673 MW; 7A313AFD CRC32;

Query Match 51.4%; Score 133; DB 1; Length 122;
Best Local Similarity 56.2%; Pred. No. 2,6e-10;
Matches 27; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Oy      1 TKLEDHLEGINIGHGVSVRGVHEPTLNKYEELKGSTGKLPRTLOXNK 48
        ::::| | | | | | | | | | | | | | | | | | | | | : |
Db      2 SQMESIEITIIINFHQYSVRGLGHDTLLQKEFKQLVKDELNFKLKKQ 49

RESULT 6
ID      S109_RAT STANDARD; PRT; 113 AA.
AC      P50116.
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DE      01-OCT-1996 (Rel. 34, Last annotation update)
DE      CALGRANULIN B (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 14)
DE      (MRP-14)
GN      S100A9 OR MRP14.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=LEWIS/N; TISSUE=PERITONEAL CAVITY;
RX      IMEDLINE: 93343942.
RA      IAMACHI T., UCHIDA I., WAHL S.M., MCCARTNEY-FRANCIS N.;
RT      "Expression and cloning of migration inhibitory factor-related
RL      protein (MRP)8 and MRP14 in arthritis-susceptible rats.";
CC      Biochem. Biophys. Res. Commun. 194:819-825(1993).
CC      -1 SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
CC      MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
-----
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CC      or send an email to license@isb-sib.ch).
DR      EMBL; L18948; AAA18214.1; -.
DR      HSSP; P04271.10WO.
DR      PROSITE; PS00018; EF_HAND; FALSE_NEG.

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RA MORI S., GOTO K., GOTO F., MUTAKAMI K., OHKAWARA S., YOSHINAGA M.,
RT "Dynamic changes in mRNA expression of neutrophils during the course
of acute inflammation in rabbits."
RL Int. Immunol. 6:149-156(1994).
CC -I- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
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CC -----
DR EMBL: AF091849; AAC61771.1; -
DR PROSITE: PS00018; EF_HAND; 1.
DR PROSITE: PS00303; S100_CABP; 1.
PFAM: PF00036; efhand; 1.
Calcium-binding; Repeat.
FT CA_BIND 1 22 SITE I (LOW AFFINITY) (POTENTIAL).
FT CA_BIND 53 64 SITE II (HIGH AFFINITY) (POTENTIAL).
FT DOMAIN 103 118 2 X 8 AA TANDEN REPEATS OF G-H-G-H-
FT REPEAT 103 110 1. G-H-S-H-
FT REPEAT 111 118 1.
SQ SEQUENCE 118 AA; 13292 MW; 0D7899DD CRC32;

Query Match 36.3%; Score 94; DB 1; Length 118;
Best Local Similarity 61.1%; Pred. No. 2.5e-05;
Matches 22; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 10 IINIGHQYVRVGHFDITLNKYLKOLGTKEPKTLQ 45
||| ||||| | : : : | ||| | :
Db 1 IINIFHQYVRVGRDLSLQKEFKOLVQKELHFLK 36

RESULT 9
M126_CHICK STANDARD; PRT; 119 AA.
AC P28318;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
RT PROTEIN MRP-126.
Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Avchosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGBORN; TISSUE-BONE MARROW;
RX MEDLINE: 92195690.
RA NAKANO T., GRAF T.;
RT "Identification of genes differentially expressed in two types of
RT v-myb-transformed avian myelomonocytic cells."
RL Oncogene 7:527-534(1992).
CC -I- TISSUE SPECIFICITY: EXPRESSED IN V-MYB-TRANSFORMED MYELOMONOCYTIC
CC CELLS.
CC -I- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
CC -----
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CC -----
DR EMBL: X61200; -; NOT_ANNOTATED_CDS.

DR HSSP; P04271; 10W0.
DR PROSITE: PS00018; EF_HAND; 1.
DR PROSITE: PS00303; S100_CABP; 1.
DR PFAM: PF00036; efhand; 1.
DR PFAM: PF01023; S_100; 1.
KW Calcium-binding.
FT CA_BIND 29 42 SITE I (LOW AFFINITY) (POTENTIAL).
FT CA_BIND 72 83 SITE II (HIGH AFFINITY) (POTENTIAL).
SQ SEQUENCE 119 AA; 14065 MW; 25718D2B CRC32;

Query Match 36.3%; Score 94; DB 1; Length 119;
Best Local Similarity 44.0%; Pred. No. 2.5e-05;
Matches 22; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

OY 1 TKLEHLEGIINIGHQYVRVGHFDITLNKYLKOLGTKEPKTLQNKDQ 50
::: ||: ||||| | ||| | ||| | : : : |
Db 12 SELEKADVIIDVPHQYSRREGDKDTLRKELKILLIEQLNKLHVKNQ 61

RESULT 10
S104_MOUSE STANDARD; PRT; 101 AA.
ID S104_MOUSE
AC P07091; P20066;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PLACENTAL CALCIUM-BINDING PROTEIN (18A2) (PEL28) (MTS1 PROTEIN)
DE (METASTATIC CELL PROTEIN).
GN S100A4 OR CAPL OR MTS1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE: 87316927.
RA JACKSON-GRUBBY L.L., SWIERGIEL J., LINZER D.I.H.;
RT "A growth-related mRNA in cultured mouse cells encodes a placental
RT calcium binding protein."
RL Nucleic Acids Res. 15:677-6690(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE: 88198109.
RA GOTO K., ENDO H., FUJITOSHI T.;
RT "Cloning of the sequences expressed abundantly in established cell
RT lines: identification of a cDNA clone highly homologous to S-100, a
RT calcium binding protein."
RL J. Biochem. 103:48-53(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89378739.
RA EBRALIDZE A., TUDCHINSKY E., GRIGORIAN M., AFANASYEVA A., SENIN V.,
RA REVAZOVA E., LUKANIDIN E.;
RT "Isolation and characterization of a gene specifically expressed in
RT different metastatic cells and whose deduced gene product has a high
RT degree of homology to a Ca2+-binding protein family."
RL Genes Dev. 3:1086-1093(1989).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE: 90236313.
RA TUDCHINSKY E.M., GRIGORIAN M.S., EBRALIDZE A.K., MISHINA N.I.,
RA LUKANIDIN E.M.;
RT "Structure of gene mts1, transcribed in metastatic mouse tumor
RT cells."
RL Gene 87:219-223(1990).
RN [5]
RP SEQUENCE OF 1-54 FROM N.A.
RX MEDLINE: 93141279.
RA TUDCHINSKY E., KRAMEROV D., FORD H.L., RESHETNYAK E., LUKANIDIN E.,
RA ZAIN S.;

[illegible]

RA	EMOTO Y KOBAYASHI R., AKATSUKA H., HIDAKA H. ;
RT	"Purification and characterization of a new member of the S-100
RL	protein family from human Placenta." ;
CC	Biochem. Biophys. Res. Commun. 182:1246-1253(1992).
CC	-1 MISCELLANEOUS: THIS PROTEIN BINDS TWO CALCIUM IONS.
CC	-1 SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
CC	MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
CC	-----
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CC	-----
DR	EMBL; X65614; CAA66566.1; -.
DR	PIR; S24146; S24146.
DR	HSP; P02638; ICFP.
DR	MIM; 600614; -.
DR	PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR	PROSITE; PS00303; S100_CABP; 1.
DR	PFAM; PF00036; efhand; 1.
DR	PFAM; PF01023; S_100; 1.
KW	Calcium-binding; Placenta.
KW	CA_BIND 19 32
FT	CA_BIND 62 73 SITE I (LOW AFFINITY).
FT	CONFLICT 32 32 SITE II (HIGH AFFINITY).
FT	CONFLICT 44 44 E -> T (IN REF. 2).
FT	CONFLICT 44 44 F -> E (IN REF. 2).
SO	SEQUENCE 95 AA; 10400 MW; EA7C214C CRC32;

```

Query Match      33.6%; Score 87; DB 1; Length 95;
Best Local Similarity 46.0%; Pred. No. 0.00015;
Matches 23; Conservative 7; Mismatches 20; Indels 0; Gaps

QY      1 TKLEDELEGIINIGHOYSVRVGHFTDLNFKYELKOLGTLKELPXTLONXKQD 50
      1:111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB      2 TELETAMGMITDVSRSYSGSEGSTQLTRGELKVLMEKELPGLQSGRDK 51

RESULT 12
S104_RAT ID S104_RAT STANDARD; PRT; 101 AA.
AC P05942;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE PLACENTAL CALCIUM-BINDING PROTEIN (NERVE GROWTH FACTOR INDUCED PROTEIN
DE 42A) (P9K).
GN S100A4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RA SEQUENCE FROM N.A.
RX MEDLINE; 88125019.
RA MASIAKOWSKI P.; SHOOPER E.M.;
RT "Nerve growth factor induces the genes for two proteins related to a
RT family of calcium-binding proteins in PC12 cells."
RT Proc. Natl. Acad. Sci. U.S.A. 85:1277-1281(1988).
RN [2]
RA SEQUENCE FROM N.A.
RX MEDLINE; 88118907.
RA BARRACLOUGH R.; SAVIN J.; DOBE S.K.; RUDLAND P.S.;
RT "Molecular cloning and sequence of the gene for p9Ka, A cultured
RT myoepithelial cell protein with strong homology to S-100, a calcium-
RT binding protein."
RT J. Mol. Biol. 198:13-20(1987).
RN [3]
RA SEQUENCE OF 3-101 FROM N.A.
RX STRAIN-OSBORNE-MENDEL; TISSUE-KIDNEY;
RX MEDLINE; 92158347.

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RA BAUDIER GLASSER N., HAGLID K., GERARD D.;  
RT "Purification, characterization and ion binding properties of human  
RL brain S100B protein.";  
RN Biochim. Biophys. Acta 790:164-173(1984).  
[4]  
RP STRUCTURE BY NMR.  
RX MEDLINE: 98179937.  
RA SMITH S.P., SHAW G.S.:  
RT "A novel calcium-sensitive switch revealed by the structure of human  
RL S100B in the calcium-bound form.";  
CC Structure 6:211-222(1998).  
CC -I- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY-  
DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH  
CC IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM  
CC ION ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY  
CC AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.  
CC -I- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR  
CC ONE ALPHA AND ONE BETA CHAIN.  
CC -I- SUBCELLULAR LOCATION: CYTOSOLASMIC.  
CC -I- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE  
CC BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES.  
CC -I- MISCELLANEOUS: IN ADDITION TO METAL-ION BINDING, THIS PROTEIN IS  
CC INVOLVED WITH THE REGULATION OF PROTEIN PHOSPHORYLATION IN BRAIN  
CC TISSUE.  
CC -I- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND  
CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.  
-----  
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DR EMBL: M59488; AAA60367.1; -.  
DR EMBL: M59487; AAA60367.1; JOINED.  
DR PIR: A03076; BCHUIB.  
DR PIR: A38364; A38364.  
DR PDB: 1UMO; 10-JUN-98.  
DR TIM: 176890; -.  
DR PROSITE: PS00018; EF_HAND_1.  
DR PROSITE: PS00303; S100_CABP; 1.  
DR PFAM: PF00036; ehand; 1.  
DR PFAM: PF01023; S_100; 1.  
KW Calcium-binding; Zinc; Metal-binding; 3D-structure.  
FT INT_MET 0  
FT MOD_RES 1 1 BLOCKED.  
FT CA_BIND 18 31 SITE 1 (LOW AFFINITY).  
FT CA_BIND 61 72 SITE II (HIGH AFFINITY).  
SQ SEQUENCE 91 AA; 10582 MW; 790F3B9 CRC32;  
  
QY 1 TKLDHLEGIINIGHOYSVRVGHFDTLNKKYLKOGSTKEPLKTLOXNXDDQ 50  
Db 1 SELERKAVALLIDVFHOYSGRGDGKHKKSELKELINNELSHFLFEIREQ 50  
  
RESULT 14  
S10B_MOUSE STANDARD; PRT; 91 AA.  
AC PS0114;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DI 01-OCT-1996 (Rel. 34, Last annotation update)  
DE S-100 PROTEIN, BETA CHAIN.  
GN S100B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Mammalia;
```

CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE: 9338628.
 RA "JIANG H., SHAH S., HILT D.C.;
 RT "Organization, sequence, and expression of the murine S100 beta gene.
 RT Transcriptional regulation by cell type-specific cis-acting
 RT regulatory elements.";
 RL J. Biol. Chem. 268:20502-20511(1993).
 CC -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY-
 CC DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH
 CC IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM
 CC ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY
 CC AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR
 CC ONE ALPHA AND ONE BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE
 CC BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
 CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
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 CC -----
 DR EMBL: L22144; AAA03075.1; -
 DR HSSP: P04271; 10MO.
 DR MGD: MGI:98217; S100B.
 DR PROSITE: PS00018; EF_HAND: 1.
 DR PROSITE: PS00303; S100_CABP; 1.
 DR PIRAM: PF00036; ehand; 1.
 DR PIRAM: PF01023; S_100; 1.
 KW Calcium-binding; Zinc; Metal-binding.
 FT INT_MET 0 BY SIMILARITY.
 FT CA_BIND 18 31 SITE 1 (LOW AFFINITY).
 FT CA_BIND 61 72 SITE 11 (HIGH AFFINITY).
 SQ SEQUENCE 91 AA; 10597 MW; 05D8C8A0 CRC32;
 Query Match 32.4%; Score 84; DB 1; Length 91;
 Best Local Similarity 40.0%; Pred. No. 0.00035;
 Matches 20; Conservative 9; Mismatches 21; Indels 0; Gaps 0;
 1 TKLEHLEGINIGHQSVRVGHEDTLNKYELKQGTKEPRTQNKXQD 50
 Db 1 SELERKAWALIDVFHQSREGDKHKLKSEKELINNELSHFLEEINEQ 50
 RESULT 15
 ID S10B_RAT STANDARD: PRT: 91 AA.
 AC P04631;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE S-100 PROTEIN, BETA CHAIN.
 GN S100B.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 85037924.
 RA KIMANO R., USUI H., MAEDA T., FUKUI T., YAMANARI N., OHTSUKA E.,
 RA IKEYHARA M., TAKAHASHI Y.;
 RT "Molecular cloning and the complete nucleotide sequence of cDNA to

RT mRNA for S-100 protein of rat brain.";
 RL Nucleic Acids Res. 12:7455-7465(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA KIMANO R., USUI H., MAEDA T., ARAKI K., KURIHARA T., YAMAKUNI T.,
 RA OHTSUKA E., IKEYHARA M., TAKAHASHI Y.;
 RT "Molecular cloning and nucleotide sequences of cDNA and genomic DNA
 RT for alpha and beta subunits of S100 protein.";
 RL Tanaguchi Symp. Brain Sci. 19:243-255(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91359841.
 RA MAEDA T., USUI H., ARAKI K., KIMANO R., TAKAHASHI Y., SUZUKI Y.;
 RT "Structure and expression of rat S-100 beta subunit gene.";
 RL Brain Res. Mol. Brain Res. 10:193-202(1991).
 RN [4]
 RP SEQUENCE OF S-91 FROM N.A.
 RX MEDLINE: 87137648.
 RA DUNN R., LANDRY C., O'HANION D., DUNN J., ALLORE R., BROWN I.,
 RA MARKS A.;
 RT "Reduction in S100 protein beta subunit mRNA in C6 rat glioma cells
 RT following treatment with anti-microtubular drugs.";
 RL J. Biol. Chem. 262:3562-3566(1987).
 RN [5]
 RP STRUCTURE BY NMR.
 RX MEDLINE: 96387197.
 RA DROHAT A.C., AMBURGEY J.C., ABILDGAARD F., STARICH M.R.,
 RA BALDISERI D.M., WEBER D.J.;
 RT "Solution structure of rat apo-S100B(beta beta) as determined by NMR
 RT spectroscopy.";
 RL Biochemistry 35:11577-11588(1996).
 RN [6]
 RP STRUCTURE BY NMR.
 RX MEDLINE: 98153156.
 RA DROHAT A.C., BALDISERI D.M., RUSTANDI R.R., WEBER D.J.;
 RT "Solution structure of calcium-bound rat S100B(beta beta) as
 RT determined by nuclear magnetic resonance spectroscopy.";
 RL Biochemistry 37:2729-2740(1998).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE: 99226808.
 RA DROHAT A.C., TJANDRA N., BALDISERI D.M., WEBER D.J.;
 RT "The use of dipolar couplings for determining the solution structure
 RT of rat apo-S100B.";
 RL Protein Sci. 8:800-809(1999).
 CC -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY-
 CC DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH
 CC IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM
 CC ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY
 CC AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR
 CC ONE ALPHA AND ONE BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE
 CC BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES.
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
 CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
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 CC -----
 DR EMBL: X01090; CAA25567.1; -
 DR EMBL: M54919; AAA42096.1; -
 DR EMBL: S53527; CAB30935.1; -
 DR EMBL: S53522; CAB30935.1; JOINED.
 DR EMBL: M15705; -; NOT_ANNOTATED_CDS.
 DR PIR: S07357; S07357.
 DR PIR: A26557; A26557.

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RESULT      1
0933395
ID          ID          PRELIMINARY;      PRT:      101 AA.
AC          AC          0933395;
DT          01-NOV-1998 (TREMBLrel. 08, Created)
DT          01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT          01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE          S100-LIKE CALCIUM BINDING PROTEIN.
GN          S100.
OS          Salvelinus fontinalis (Brook trout).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC          Neopterygii; Teleostei; Euteleostei; Protacanthopterygii;
OC          Salmoniformes; Salmonidae; Salvelinus.
RN          [1]
RP          SEQUENCE FROM N.A.
RC          TISSUE-OVULATORY OVARY;
RA          BOBE J.M., GOERTZ F.W.;
RT          "Downregulation of a S100-like calcium binding protein in the brook
RL          trout ovary following ovulation."
RL          Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN          [2]
RP          SEQUENCE FROM N.A.
RC          TISSUE-OVULATORY OVARY;
RA          LANGENAU D.M., GOERTZ F.W.;
RL          Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR          EMBL: AF077613; AAC28367.1; -.
DR          HSSP: P02633; 1BOC.
DR          PROSITE: PS00303; S100_CABP; 1.
DR          PFM: PFO0036; efhnd; 1.
DR          PFM: PFO1023; S_100; 1.
SQ          SEQUENCE      101 AA; 11285 MW;  DDBFC2E8 CRC32;
QY          Query Match      34.7%;      Score 90;      DB 13;      Length 101;
          Best Local Similarity      38.8%;      Pred. No. 0.0008;
          Matches      19;      Conservative      13;      Mismatches      17;      Indels      0;      Gaps      0;
Db          1 TKLEDHLEGINIGHOXYSVRYGHFDTLINKYKLOUGTKELPKTQXKD 49
          :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
          3 SQLESMESLITVFRHYADKDGDCNTLSKRLKELMOTELASFLKSQND 51

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001720 ID 001720 PRELIMINARY; PRT; 591 AA.
AC 001720;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE FILAGGRIN PRECURSOR (PROFILAGGRIN) (FRAGMENT).
GN FLG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA.
RX MEDLINE: 93054736.
RA PRESLAND R.B., HAYDOCK P.V., FLECKMAN P., NIRUNSUJIRI W., DALE B.A.;
RT "characterization of the human epidermal profilaggrin gene. Genomic
RT organization and identification of an S-100-like calcium binding
RT domain at the amino terminus";
RL J. Biol. Chem. 267:23772-23781(1992).
CC -1- FUNCTION: AGGREGATES KERATIN INTERMEDIATE FILAMENTS AND PROMOTES
CC DISULFID-BOND FORMATION AMONGST THE INTERMEDIATE FILAMENTS DURING
CC TERMINAL DIFFERENTIATION OF MAMMALIAN EPIDERMIS.
CC -1- PTM: FILAGGRIN IS INITIALLY SYNTHESIZED AS A LARGE, INSOLUBLE,
CC HIGHLY PHOSPHORYLATED PRECURSOR CONTAINING MANY TANDEM COPIES OF
CC 324 AA. THE PRECURSOR IS DEPOSITED AS KERATOHYALIN GRANULES.
CC DURING TERMINAL DIFFERENTIATION IT IS DEPHOSPHORYLATED &
CC PROTEOLYTICALLY CLEAVED.
CC -1- POLYMORPHISM: A NUMBER OF PROFILAGGRIN ISOFORMS HAVE BEEN FOUND
CC WHICH DIFFER BOTH IN SEQUENCE AND IN THE NUMBER OF FILAGGRIN
CC REPEATS.
CC EMBL: L01089; AAA60177.1; -.
CC DR EMBL: L01090; AAA60176.1; -.
CC DR HSSP: P30801; ICNP.
CC DR MIM: 135940; -.
CC PRAM: PRQ0036; efband. 1.
CC PRAM: PF01023; S_100; 1.
CC KW Polymorphism.
CC FT PROPEP 1 293 POTENTIAL.
CC FT CHAIN 294 467 FILAGGRIN.
CC FT PROPEP 468 474 POTENTIAL.
CC FT CHAIN 475 >591 FILAGGRIN.
CC FT CA_BIND 19 32 SITE I (BY SIMILARITY).
CC FT NON_TER 62 73 SITE II (BY SIMILARITY).
CC FT SEQUENCE 591 AA; 66366 MW; 747C0F83 CRC32;
SQ

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Query Match 31.3%; Score 81; DB 4; Length 591;
 Best Local Similarity 42.6%; Pred. No. 0.066;
 Matches 20; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

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OY 3 LEDHLEGIINIGHQYSVRGHFDLTKYELKGLTKELPKTLQXKD 49
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 4 LLENIFALINLFKQYSKKDKNTDLSKKELEKEFRQILKNPDD 50

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RESULT 3
 ID 005331 PRELIMINARY; PRT; 1218 AA.
 AC 005331;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
 DE FILAGGRIN (PROFILAGGRIN) (FRAGMENT).
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-FORESKIN.
 RX MEDLINE: 93109348.
 RA MARKOVA N.G., MAKEKOV L.N., CHIRYEV C.C., GAN S.-O., IDLER W.W.,

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RA STEINERT P.M.;
RT "Profilaggrin is a major epidermal calcium-binding protein.";
RL Mol. Cell. Biol. 13:613-625(1993).
CC -1- FUNCTION: AGGREGATES KERATIN INTERMEDIATE FILAMENTS AND PROMOTES
CC DISULFID-BOND FORMATION AMONGST THE INTERMEDIATE FILAMENTS DURING
CC TERMINAL DIFFERENTIATION OF MAMMALIAN EPIDERMIS.
CC -1- PTM: FILAGGRIN IS INITIALLY SYNTHESIZED AS A LARGE, INSOLUBLE,
CC HIGHLY PHOSPHORYLATED PRECURSOR CONTAINING MANY TANDEM COPIES OF
CC 324 AA. THE PRECURSOR IS DEPOSITED AS KERATOHYALIN GRANULES.
CC DURING TERMINAL DIFFERENTIATION IT IS DEPHOSPHORYLATED &
CC PROTEOLYTICALLY CLEAVED.
CC -1- POLYMORPHISM: A NUMBER OF PROFILAGGRIN ISOFORMS HAVE BEEN FOUND
CC WHICH DIFFER BOTH IN SEQUENCE AND IN THE NUMBER OF FILAGGRIN
CC REPEATS.
CC EMBL: M96943; AAA36487.1; -.
CC DR HSSP: P30801; ICNP.
CC PRAM: PRQ0036; efband. 1.
CC PRAM: PF01023; S_100; 1.
CC KW Phosphorylation; Polyprotein; Developmental protein; Calcium-binding;
CC KW Polymorphism.
CC FT CA_BIND 19 32 SITE I (BY SIMILARITY).
CC FT CA_BIND 62 73 SITE II (BY SIMILARITY).
CC FT NON_TER 1218 1218
CC FT SEQUENCE 1218 AA; 133605 MW; F52F278C CRC32;
SQ

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Query Match 29.7%; Score 77; DB 4; Length 1218;
 Best Local Similarity 45.0%; Pred. No. 0.43;
 Matches 18; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

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OY 10 IINIGHQYSVRGHFDLTKYELKGLTKELPKTLQXKD 49
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 11 IINLFNEYSKKDKNTDLSKKELEKEFRQILKNPDD 50

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RESULT 4
 ID 09YH57 PRELIMINARY; PRT; 217 AA.
 AC 09YH57;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
 DE P26OLF.
 GN P26OLF CDNA.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 OC Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OLFACTORY;
 RX MEDLINE: 99008915.
 RA MWA N., KOBAYASHI M., TAKAMATSU K., KAWAMURA S.;
 RT "Purification and molecular cloning of a novel calcium-binding
 RT protein, p26OLF, in the frog olfactory epithelium";
 RL Biochem. Biophys. Res. Commun. 251:860-867(1998).
 DR EMBL: D50333; BAA34388.1; -.
 DR HSSP: P08206; 1BT6.
 DR SEQUENCE 217 AA; 24494 MW; 90FB7718 CRC32;
SQ

Query Match 25.1%; Score 65; DB 13; Length 217;
 Best Local Similarity 30.6%; Pred. No. 1.8;
 Matches 15; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

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OY 1 TKLEHLEGIINIGHQYSVRGHFDLTKYELKGLTKELPKTLQXKD 49
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 10 TEMERSERKILTFVRYAGKEGNTSMNFEQFMNAELGSEPTKXKD 58

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RESULT 5
 ID 09X1L8 PRELIMINARY; PRT; 438 AA.
 AC 09X1L8;
 DT 01-NOV-1999 (TEMBLrel. 01, Created)
 DT 01-NOV-1999 (TEMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 01, Last sequence update)
 DE FILAGGRIN (PROFILAGGRIN) (FRAGMENT).
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-FORESKIN.
 RX MEDLINE: 93109348.
 RA MARKOVA N.G., MAKEKOV L.N., CHIRYEV C.C., GAN S.-O., IDLER W.W.,

DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)
DE FIXC PROTEIN.
GN TM1532.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 99287316.
RA NELSON K.E., CLAYTON R.A., GILL S.R., GRINN M.L., DODSON R.J.,
RA HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
RA MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
RA STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
RA HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
RA SMITH H.O., VENTER J.C., FRASER C.M.;
RT "Evidence for lateral gene transfer between Archaea and bacteria from
genome sequence of Thermotoga maritima."
Nature 399:323-329(1999).
[2]
SEQUENCE FROM N.A.
RA NELSON K.E., CLAYTON R.A., GILL S.R., GRINN M.L., DODSON R.J.,
RA HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
RA MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
RA STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
RA HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
RA SMITH H.O., VENTER J.C., FRASER C.M.;
RT Submitted (JUN-1999) to the EMBL/genbank/DBJ databases.
DR EMBL: AF001800; AAD36599.1; -
SQ SEQUENCE 438 AA; 48974 MW; F8F8008A CRC32;

Query Match 23.4%; Score 60.5; DB 2; Length 438;
Best Local Similarity 29.3%; Pred. No. 13;
Matches 17; Conservative 11; Mismatches 15; Indels 15; Gaps 2;

OY 8 EGIINIGHQ-----YSVRVGHFDLTKYELKQGTKEPKPT-----LQNXKQD 50
ID 86 EGVIRKIGHNVEMKENPNAFTVLRFANFDMQFQVEVAKAGLLIPKRYDEFLNENKGE 143
DB 86 EGVIRKIGHNVEMKENPNAFTVLRFANFDMQFQVEVAKAGLLIPKRYDEFLNENKGE 143
RESULT 6
AC P79342 PRELIMINARY; PRT; 98 AA.
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)
DE 8KDA AMLEXANOX-BINDING PROTEIN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RA OYAMA Y., SHISHIBORI T., MATSUTOMO M., YAMASHITA K., MAETA H.,
RA KOBAYASHI R.;
RT "Molecular cloning of a new 8kDa protein, isolated with Amlexanox
couple d column chromatography."
Submitted (MAR-1997) to the EMBL/genbank/DBJ databases.
DR EMBL: AB001567; BAA19411.1; -
DR HSSP: P30801; ICNP.
DR PFAM: PF01023; S_100; 1.
SQ SEQUENCE 98 AA; 11233 MW; 70331499 CRC32;

Query Match 23.2%; Score 60; DB 6; Length 98;
Best Local Similarity 30.4%; Pred. No. 3;
Matches 14; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

OY 1 TKIEDHLEGIINIGHOYSVRVGHFDLTKYELKQGTKEPKPTLQNXKQD 46
ID 1 TKIEDHLEGIINIGHOYSVRVGHFDLTKYELKQGTKEPKPTLQNXKQD 46
DB 7 TELEAAIEIVTVTTFEFAGREGKRSLSYVEFKELVTOOLPHILKD 52

RESULT 7
ID 0921B5 PRELIMINARY; PRT; 1238 AA.
AC 0921B5;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)
DE S-LAYER-RTX PROTEIN.
GN CSXB.
OS Wollweilla recta.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC33238;
RA BRAUN M., FREY J., KUHNERT P.;
RT "Characterization of antigenic bistructural S-layer-RTX proteins from
Campylobacter rectus."
RT Submitted (NOV-1997) to the EMBL/genbank/DBJ databases.
DR EMBL: AF035192; AAD02003.1; -
DR PROSITE: P500330; HEMOLYSIN_CACTIUM; 11.
SQ SEQUENCE 1238 AA; 130821 MW; F868B05C CRC32;

Query Match 22.6%; Score 58.5; DB 2; Length 1238;
Best Local Similarity 26.7%; Pred. No. 73;
Matches 16; Conservative 10; Mismatches 23; Indels 11; Gaps 1;

OY 2 KLEHLEGIINIG-----HOYSVRVGHFDLTKYELKQGTKEPKPTLQNXKQD 50
ID 606 RIEGDKDITLDGGEGVDLTLEDHEDIDLNALQADWIKNFELLDGSGNNPKTLRLTFQ 665
DB 606 RIEGDKDITLDGGEGVDLTLEDHEDIDLNALQADWIKNFELLDGSGNNPKTLRLTFQ 665
RESULT 8
AC 050262 PRELIMINARY; PRT; 193 AA.
ID 050262;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, last annotation update)
DE APPLE PROLIFERATION, STRAIN AT NITROREDUCTASE LIKE PROTEIN
DE (FRAGMENT).
OS Phytoplasma sp.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Actinobacteria; Actinomycetales; Phytoplasma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-APPLE PROLIFERATION, STRAIN AT;
RA SAILLARD C., JARAUSCH W., DOSA F., BOYE J.;
RT Submitted (APR-1994) to the EMBL/genbank/DBJ databases.
DR EMBL: L22217; AAA18507.1; -
FT NON_TER 193
SQ SEQUENCE 193 AA; 23105 MW; 503C498C CRC32;

Query Match 21.6%; Score 56; DB 2; Length 193;
Best Local Similarity 30.0%; Pred. No. 19;
Matches 12; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

OY 10 IINIGHOYSVRVGHFDLTKYELKQGTKEPKPTLQNXKQD 49
ID 10 IINIGHOYSVRVGHFDLTKYELKQGTKEPKPTLQNXKQD 49
DB 133 IIDVRNHYEYOLGHRKNAINPKIKNF--RELPLWENKNK 170

Query Match 21.6%; Score 56; DB 2; Length 193;
Best Local Similarity 30.0%; Pred. No. 19;
Matches 12; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

OY 10 IINIGHOYSVRVGHFDLTKYELKQGTKEPKPTLQNXKQD 49
ID 10 IINIGHOYSVRVGHFDLTKYELKQGTKEPKPTLQNXKQD 49
DB 133 IIDVRNHYEYOLGHRKNAINPKIKNF--RELPLWENKNK 170

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DE BETA-XYLIDASE PRECURSOR (EC 3.2.1.37).
GN BXL1.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
OC Hypocreales; Hypocreaceae; Hypocrea.
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN-RUTC-30.
RA MARCOLLES-CLARK E.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RP STRAIN-RUTC-30.
RA MEDLINE; 96434473.
RX MARCOLLES-CLARK E., TENKANEN M., NAKARI-SETALA T., PENTTILA M.;
RT "Cloning of genes encoding alpha-L-arabinofuranosidase and beta-
RT xylidase from Trichoderma reesei by expression in Saccharomyces
RT cerevisiae."
RL Appl. Environ. Microbiol. 62:3840-3846(1996).
RN [3]
RC SEQUENCE FROM N.A.
RP STRAIN-RUTC-30.
RA MARCOLLES-CLARK E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; 269257; CAB3248.1;
KW Signal; Hydrolase; Glycosidase.
FT SIGNAL 1 20
FT CHAIN 21 797
FT SEQUENCE 797 AA; 87190 MW; 285BAB5 CRC32;

Query Match 21.6%; Score 56; DB 3; Length 797;
Best Local Similarity 48.0%; Pred. No. 89;
Matches 12; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

QY 19 VRYGHFDLTKYELKQGTKEPKT 43
DB 378 VRLGYFDKKNQY--RSLGWRDVKVT 400

RESULT 10
077385 PRELIMINARY; PRT; 1553 AA.
AC 077385;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 12, Last annotation update)
DE PFC0755C. PROTEIN.
RP PFC0755C.
RC Plasmodium falciparum.
RA Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN-3D7.
RA MURPHY L., LANSON D., BARRELL B.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; 298551; CAB1141.1;
DR HSSP; P24941; IAO1.
DR PFAW; P24941; PKinase; 2.
SQ SEQUENCE 1553 AA; 182218 MW; E3EA569A CRC32;

Query Match 21.6%; Score 56; DB 5; Length 1553;
Best Local Similarity 28.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 9; Mismatches 11; Indels 16; Gaps 2;

QY 4 EDHLE-----INIGHOY--SVRVGHFDLTKYELKQGT 37
DB 598 DDHFEKLEFKPRICVYVNNNGKNDYNNLSVSHYDVEKRRVNLGS 647

RESULT 11

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Q28714
ID Q28714 PRELIMINARY; PRT; 73 AA.
AC Q28714;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE MACROPHAGE MIGRATION INHIBITORY FACTOR-RELATED PROTEIN-8 (FRAGMENT).
GN MRP-8.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN-NEW ZEALAND WHITE;
RX MEDLINE; 94198229.
RA MORI S., GOTO K., GOTO F., MURAKAMI K., OKAMURA S., YOSHINAGA M.;
RT "Dynamic changes in mRNA expression of neutrophils during the course
RT of acute inflammation in rabbits."
RL Int. Immunol. 6:149-156(1994).
DR EMBL; D17405; BAA04228.1;
DR HSSP; P02633; IBOD.
DR PFAW; PF01023; S_100; 1.
FT NON_TER 73
FT SEQUENCE 73 AA; 8381 MW; ADF76812 CRC32;

Query Match 21.0%; Score 54.5; DB 6; Length 73;
Best Local Similarity 37.2%; Pred. No. 10;
Matches 16; Conservative 9; Mismatches 15; Indels 3; Gaps 2;

QY 1 TKLEHLEGIINIGHOYVRVGHFDLTKY-ELKQGTKEPK 42
DB 3 TLENSLNSIIFVYHKCSLEKNGYQAL--YGDLLKRLATECPQ 43

RESULT 12
P96025
ID P96025 PRELIMINARY; PRT; 260 AA.
AC P96025;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE INSERTION SEQUENCE IS257 AND ORF22 PROTEIN (FRAGMENT).
OS Staphylococcus simulans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RC SEQUENCE FROM N.A.
RP THOMAS G., GOERTZ F.;
RA EMBL; U66882; AAB39603.1;
DR PFAW; PF00325; crp; 1.
FT NON_TER 260
FT SEQUENCE 260 AA; 30271 MW; 8549C420 CRC32;

Query Match 21.0%; Score 54.5; DB 2; Length 260;
Best Local Similarity 30.2%; Pred. No. 40;
Matches 16; Conservative 12; Mismatches 14; Indels 11; Gaps 4;

QY 3 LEDH-----LEGIINIGHOYVRVGHFDLTKY-ELKQGTKEPK 44
DB 8 LEEHATFDSIQEMDNTVROYNKISKTHYETLNLKQYSCVIGVSHDKIKTI 60

RESULT 13
O13378
ID O13378 PRELIMINARY; PRT; 452 AA.
AC O13378;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE ACYL-COA DESATURASE 1 (EC 1.14.99.5) (STEAROYL-COA DESATURASE 1)

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DE (FATTY ACID DESATURASE 1).
GN OLE1.
OS Mucor rouxii.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC Mucor.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 24905;
RA LAOTENG K., ANJARD C., CHEEVADHANARAK S., TANTICHAROEN M.,
RA RACHADAMONG S.;
Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: STEAROYL-COA + AH(2) + O(2) -> CLEOYL-COA + A +
CC 2 H(2)O.
CC -1- COFACTOR: IRON.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
DR EMBL: AF026401; AAB82294.1; -.
DR HSSP: P00173; 1IEU.
DR PROSITE: PS00476; FATTY_ACID_DESATUR_1; 1.
DR PFAM: PF01069; Desaturase; 1.
DR PRINTS: PR00075; FACDSATRASE.
KM Oxidoreductase; Fatty acid biosynthesis; Iron; Membrane;
KW Endoplasmic reticulum.
SQ SEQUENCE 452 AA; 51963 MW; B8F5E48 CRC32;

Query Match 21.0%; Score 54.5; DB 3; Length 452;
Best Local Similarity 28.8%; Pred. No. 73;
Matches 15; Conservative 6; Mismatches 14; Indels 17; Gaps 2;

QY 8 EGIINIGHQY-----SVRVGHEDTLN-----KYLKQLGTKEPK 42
DB 263 EGYHNFHHPQPDYRNAIKFGQYDPTKMKIIVLSWFGIAYELKQFPINNEYVK 314

RESULT 14
O49356 PRELIMINARY; PRT; 444 AA.
AC O49356;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DE 01-JUN-1998 (TEMBLrel. 06, Last annotation update)
DE FERREDOXIN--NADP+ REDUCTASE - LIKE PROTEIN.
GN F10M6.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RA BRYAN M., WEICHELSEKARTNER M., FARTMANN B., GRANDERATH K., DAUNER D.,
RA HERZL A., NEUMANN S., HOHEISEL J., MEWES H.W., MAYER K., SCHUELLER C.;
RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL021811; CAA16955.1; -.
SQ SEQUENCE 444 AA; 48698 MW; 3F3BB4A2 CRC32;

Query Match 20.8%; Score 54; DB 10; Length 444;
Best Local Similarity 30.4%; Pred. No. 82;
Matches 14; Conservative 7; Mismatches 15; Indels 10; Gaps 2;

QY 6 HLEGI-----INGHOYSVRVGHEDTLN-KYLKQLGTKEPK 41
DB 267 HVSQVNLQKITLESVGTGQIAVGTGEFEDLNCMVLAIGKVSVP 312

RESULT 15
O04053 PRELIMINARY; PRT; 625 AA.
AC O04053;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)

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DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE D9461.13P.
GN D9461.13.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RA DIETRICH F.S.;
Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA DIETRICH F.S., MULLIGAN J., ALLEN E., ARAUJO R., AVILES E., BERNO A.,
RA CARPENTER J., CHEN E., CHERRY J.M., CHUNG E., DUNCAN M.,
RA HUNICKER-SMITH S., HYMAN R., KOMP C., LASHKARI D., LEW H., LIN D.,
RA MOSEDALE D., NAKAHARA K., NAMATH A., OEFNER P., OH C., PEREL F.X.,
RA ROBERTS D., SCHRAMM S., SCHROEDER M., SHOKREN T., SHROFF N.,
RA WINANT A., YELTON M., BOTSTEIN D., DAVIS R.W.;
Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA DIETRICH F.S.;
Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA JIA Y., CHERRY J.M.;
Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U33007; AAB64858.1; -.
DR PFAM: PF00787; PX; 1.
SQ SEQUENCE 625 AA; 70740 MW; 29A8257F CRC32;

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Query Match 20.8%; Score 54; DB 3; Length 625;
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 8; Mismatches 10; Indels 10; Gaps 2;

QY 14 GHQYSVRVG---HFDT-----LNKYLKQLGTKEPKTLQ 45
DB 509 GHQNEIHIGASKLNKYSTPTMNLKLEIKQLTQERSKQIK 550

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Search completed: March 14, 2000, 15:47:29
 Job time: 623 sec

